

02 4/16

CR7A

Access DB# 91465

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: K. Cochrane Carlson Examiner #: 701/46 Date: 4-8-03
 Art Unit: 1653 Phone Number: 308 0034 Serial Number: 09709585
 Mail Box and Bldg/Room Location: 9301 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search and interference
 search Seq ID NO:2, also 15 consecutive
 aa of Seq ID NO:2.

This is a no issue application. The
 CR7 is in SN 08/401530

POINT OF CONTACT:
 PAUL SCHULWITZ
 TECHNICAL INFO. SPECIALIST
 GM1 8806 TEL. (703) 305-1954

Thanks
 Karen

4-14

- Mark Spencer says to search the patent 5,834,590
 see attached

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) <u>2</u>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>4/16</u>	Bibliographic _____	Dr. Link _____
Date Completed: <u>4/16</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>5</u>	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>5</u>	Other _____	Other (specify) _____

Carlson, Karen

From: Spencer, Mark
Sent: Monday, April 14, 2003 10:36 AM
To: Carlson, Karen
Subject: RE: 09/709585 is a re-issue of 08/401530

Karen,
The sequences for 08/401,530 can be searched in the issued database under patent number 5834590. I checked the database and the sequences are there. Let Mary Hale and I know if you have any further trouble.

Thanks,
Mark

-----Original Message-----

From: Carlson, Karen
Sent: Monday, April 14, 2003 8:06 AM
T : Spencer, Mark
Subject: 09/709585 is a re-issue of 08/401530

Hi Mark,
I need to re-search a sequence in '530 for a reissue application. Leonard in STIC says that '530 does not have a CRF and the sequences are in a public database and not searchable by STIC from that venue.

Can this be corrected?

Thanks!

Karen Cochrane Carlson
AU 1653
CM1 10A07
Mailbox CM1 9B01

GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OK protein - protein search, using sw model

Run on: April 16, 2003, 10:40:45 ; Search time 36 Seconds

(without alignments)
644.045 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 1 MLEPTLCRMGMMLISCLMFL.....QKWRDPCNELPYCKFRV 174

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.Geneseq.101002:*

1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	958	100.0	174	AA98525	Hamster islet neog
2	958	100.0	175	AA64790	INGAP protein frag
3	605.5	63.2	175	AA54097	Mus PAP. Mus mu
4	593	61.9	175	AA95089	Reg-2 protein. Ra
5	593	61.9	175	AA18614	Amino acid sequenc
6	572	59.7	175	AA54098	Mus PAP. Mus mu
7	572	59.7	175	AA57117	Human Pancreatitis
8	572	59.7	183	AA54568	Human cancer assoc
9	566	59.1	174	AA14795	Fragment A3 from h
10	557	58.1	175	AAW71682	Human pancreatitis

11	557	58.1	175	AA41755	Human PRO162 prote
12	557	58.1	175	AA44311	Human PRO162 (UNO4
13	557	58.1	175	AAU29235	Human PRO polypept
14	557	58.1	175	AB95482	Human angiogenesis
15	557	58.1	175	AB84876	Human PRO162 prote
16	557	58.1	175	AA14797	Rat pancreatitis a
17	525.5	54.9	175	AA05904	Bovine pancreatic
18	522	54.5	210	ABG18688	Novel human diagno
19	484	50.5	158	AA14796	Fragment A2 from r
20	408.5	42.6	174	AA54301	Human pancreatit
21	395.5	41.3	165	AA81513	Sequence encoded b
22	395.5	41.3	165	AA83188	Sequence encoded b
23	395.5	41.3	165	AA85289	Rat reg protein.
24	394.5	41.2	165	AA84615	Rat reg protein.
25	387	40.4	121	ABG18687	Novel human diagno
26	386.5	40.3	165	AA84535	MUREG-1. Mus musc
27	386.5	40.3	174	AA843737	Human cancer assoc
28	386	40.3	173	AA84536	MUREG-2. Mus musc
29	385.5	40.2	166	AA85288	Human reg protein.
30	385.5	40.2	166	AA81653	Human colon associ
31	385.5	40.2	166	AA81666	Human colon associ
32	379.5	39.6	166	AA81666	Human reg protein.
33	379.5	39.6	166	AA81666	Human reg protein.
34	362.5	37.8	146	AA86594	Rat reg protein (G
35	354.5	37.0	144	AA86595	Rat reg protein (G
36	342.5	35.8	147	AA86425	Human reg protein
37	341.5	35.6	146	AA86591	Human reg protein
38	333.5	34.8	144	AA86592	Human reg protein
39	323.5	33.8	133	AA86593	Rat reg protein (I
40	303.5	31.7	133	AA86593	Human reg protein
41	257.5	26.9	294	ABG01855	Novel human diagno
42	257.5	26.9	406	ABG03060	Novel human diagno
43	257.5	26.9	558	ABG00465	Novel human diagno
44	250	26.1	106	AA844108	Human cancer assoc
45	209.5	21.9	240	ABG20353	Novel human diagno

ALIGNMENTS

RESULT 1	AA98525	standard; Protein, 174 AA.
AA98525	AA98525	
AC	AA98525	
XX		
DT	18-APR-1997	(first entry)
XX		
DE	Hamster islet neogenesis associated protein.	
XX		
KW	Hamster islet neogenesis associated protein; INGAP; pancreas; endocrine;	
KW	proliferation; pancreatic tissue; cell; epithelium; homology;	
KW	differential display method; open reading frame; liver; adenocarcinoma;	
KW	pancreatitis associated protein; lithostathine; pancreatic stone protein;	
KW	beta-cell; regeneration; insulin; diabetes; mammal.	
XX		
OS	Cricetulus sp.	
XX		
PN	WO966215-A1.	
PD	29-AUG-1996.	
XX		
PF	12-FEB-1996;	96WO-US01528.
XX		
PR	07-NOV-1995;	95US-0006271.
XX	22-FEB-1995;	95US-0401530.
PA	(EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.	
XX		
PI	Duguid WP, Pittenger GL, Rafaeloff R, Rosenberg L;	
XX	Vank A;	
XX		
DR	WPI, 1996-402318/40.	

DR N-PSDB; AAT36612.
 XX Mammalian islet neo:genesis associated protein - isolated by
 PT stimulating mammalian pancreas by wrapping in cellophane, for
 PT- treatment of diabetes, etc
 XX-
 PS Claim 2; Page 26; 50pp; English.
 CC
 CC This is the amino acid sequence of the hamster islet neogenesis
 CC associated protein (INGAP). The gene is isolated from pancreatic cells
 CC which are induced to proliferate upon wrapping pancreatic tissue in
 CC cellophane. Wrapping of the pancreas stimulate proliferation of new
 CC endocrine cells which appear from duct epithelium. The INGAP gene was
 CC isolated from a cDNA library constructed from mRNA purified from
 CC cellophane wrapped hamster pancreas using a differential display method
 CC to compare genes expressed in cellophane-wrapped and control pancreas
 CC The gene contains an open reading frame which encodes a protein of 175
 CC amino acids. The protein has structural homology to the pancreatic
 CC associated protein (PAP)/HIP family of genes which is associated with
 CC pancreatic or liver adenocarcinoma, and to the Reg/PSP/lithostatine
 CC (PSP = pancreatic stone protein) family of gene which has been shown to
 CC stimulate pancreatic beta cell growth and may be involved in pancreatic
 CC islet regeneration. The protein can be used to stimulate islet cell
 CC proliferation in (non-)insulin dependent diabetic mammals.

SO Sequence 174 AA;

Query Match 100.0%; Score 958; DB 17; Length 174;
 Best Local Similarity 100.0%; Pred. No. 2.8e-88;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPTLCRSMWMLSCIMFLSWVEGEESQKLPSSRITCPOGSVAVGSCYSLILIPQW 60
 DB 1 MLPTLCRSMWMLSCIMFLSWVEGEESQKLPSSRITCPOGSVAVGSCYSLILIPQW 60
 OY 61 SNAELSCQMHEFSGHLAFLSTGEITFVSSLVKNSLTAIYIWIGLHDPHGTLPNGSGWK 120
 DB 61 SNAELSCQMHEFSGHLAFLSTGEITFVSSLVKNSLTAIYIWIGLHDPHGTLPNGSGWK 120
 OY 121 WSSSNVLTFFYNNERNPSTIADRGYCAVLQKSGFQKRPDNCENELPYICKRFV 174
 DB 121 WSSSNVLTFFYNNERNPSTIADRGYCAVLQKSGFQKRPDNCENELPYICKRFV 174

RESULT 2

AAM64790
 ID AAM64790 standard; Protein; 175 AA.

XX AAM64790;

XX 18-NOV-1998 (first entry)

XX INGAP protein fragment.

XX INGAP; islet neogenesis-associated protein; treatment; diabetes;
 KW host cell.

XX Unknown.

OS US5804421-A.

PN 08-SEP-1998.

PD 12-AUG-1997; 97US-0909725.

PF 12-AUG-1997; 97US-0909725.

PR 30-OCT-1996; 96US-0741096.

XX (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.

XX Barlow SM, Pittenger GL, Rafaeloff-Phail R, Vink AI;

XX WPI; 1998-505656/43.

XX Expression of islet neogenesis-associated protein - from recombinant
 PT construct lacking signal peptide, useful in the treatment of
 PT diabetes
 PT-
 XX-
 PS Claim 1; Column 19-20; 14pp; English.

CC This sequence represents INGAP, an islet neogenesis-associated protein.
 CC This sequence is used in the construction of a recombinant construct
 CC having a coding sequence lacking a signal sequence and which is operably
 CC linked to transcription and translation initiation sites. This construct
 CC in a host cell is useful for producing recombinant mature INGAP, which
 CC is useful in the treatment of diabetes. High levels of INGAP expression
 CC can be achieved in bacterial and eukaryotic cells by removing the signal
 CC peptide as it is possibly toxic to cells.

SO Sequence 175 AA;

Query Match 100.0%; Score 958; DB 19; Length 175;
 Best Local Similarity 100.0%; Pred. No. 2.8e-88;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPTLCRSMWMLSCIMFLSWVEGEESQKLPSSRITCPOGSVAVGSCYSLILIPQW 60
 DB 2 MLPTLCRSMWMLSCIMFLSWVEGEESQKLPSSRITCPOGSVAVGSCYSLILIPQW 61
 OY 61 SNAELSCQMHEFSGHLAFLSTGEITFVSSLVKNSLTAIYIWIGLHDPHGTLPNGSGWK 120
 DB 62 SNAELSCQMHEFSGHLAFLSTGEITFVSSLVKNSLTAIYIWIGLHDPHGTLPNGSGWK 121
 OY 121 WSSSNVLTFFYNNERNPSTIADRGYCAVLQKSGFQKRPDNCENELPYICKRFV 174
 DB 122 WSSSNVLTFFYNNERNPSTIADRGYCAVLQKSGFQKRPDNCENELPYICKRFV 175

RESULT 3

AAR54097
 ID AAR54097 standard; Protein; 175 AA.

XX AAR54097;

XX 01-FEB-1995 (first entry)

XX Mouse PAP.

XX Pancreatitis-Associated Protein; PAP; mouse; human; bacteria;
 KW aggregation; antibacterial; primer; PCR.

XX Mus musculus.

OS JP06135998-A.

PN 17-MAY-1994.

PD 22-OCT-1992; 92JP-0284765.

PF 22-OCT-1992; 92JP-0284765.

PR 22-OCT-1992; 92JP-0284765.

XX (SHIO) SHIONOGI & CO LTD.

PA WPI; 1994-197103/24.

DR N-PSDB; AAO64171.

XX Human and mouse pancreatitis-associated protein (PAP) - useful
 PT for prepn. of proteinaceous antibacterial agent

PS Claim 1-6; Page 5-6; 7pp; Japanese.

CC PAP DNA has a high bacteria-aggregating activity and is useful for
 CC the prepn. of PAP which can act as a proteinaceous antibacterial
 CC agent. Total RNA was isolated from mouse. It was hybridised with a
 CC modified salmon spermatozoa DNA and known rat PAP cDNA as a probe.
 CC Two primers are given in AAO64173-74.

XX	Sequence	175 AA:	63.2%:	Score 605.5:	DB 15:	Length 175:
SO	Query Match		60.7%:	Pred. No. 7.5e-53:		
	Best Local Similarity					
	Matches 105:	Conservative	29:	Mismatches 38:	Indels 1:	Gaps 1:
QY	1	MLPNTLCR-MSMMLLSCTMLFSLWGEESOKKLPSSRINCPGSAVYAGSYCYLLIPQT	59			
DB	1	MLPPTACSVSMMLLSCTMLLSQVGEDSLKNIPSAIRICPKGSAVGYCYALPQIPQT	60			
QY	60	WSNAELSCOMHMSGHLLPFLSTGELTPFVSLVKNLSLTAAQYIWMIGIHDPDSEHTLPGSGW	119			
DB	61	WDAELACCKRRPGGHLYSVLNSAEKSLFSSMKKRRGNISQYIWTIGLHDPFLAEFRGSGW	120			
QY	120	KWSSSNVLTFTYMERNPSTADRGYCAVLISQKSGFQKRWDFENCENELPYICKF	172			
DB	121	EWSNDVNYTFYMERNPSTALDRACGSLSTRASGFLKRWDMTCCEKLPYVCKF	173			

XX	RESULT 4
ID	AAM95089
AC	AAM95089 standard; Protein; 175 AA.
XX	
AC	AAM95089;
XX	
DT	20-MAY-1999 (first entry)
XX	
DE	Reg-2 protein.
XX	
KW	Reg-2; Schwann cell mitogen; repair; regenerate; neuronal cell; tissue;
RN	glial growth factor; neuroglin.
XX	
OS	Rattus sp.
XX	
PN	GB2329335-A.
XX	
PD	24-MAR-1999.
XX	
PF	16-SEP-1998; 98GB-0020193.
XX	
PR	17-SEP-1997; 97GB-0019796.
XX	
PA	(MEDI-) MEDICAL RES COUNCIL.
XX	
PI	Hunt SP, Livey FJ;
XX	
DR	WPI: 1999-156299/14.
XX	N-PSDB: AAX26126.
PT	Use of a protein (Reg-2) to manufacture a Schwann cell mitogen. - to
PT	repair and/or regenerate neuronal cells or tissue, either in vivo,
PT	or in vitro and then introduced into subject
XX	
PS	Claim 1; Page 24; 33pp; English.
XX	
CC	The invention relates to the use of a protein (Reg-2) or its variant,
CC	derivative or homologue, to manufacture a Schwann cell mitogen. Reg-2 is
CC	used to repair and/or regenerate neuronal cells or tissue. Neuronal cells
CC	or tissue may be repaired and/or regenerated either in vivo, or in vitro
CC	and then introduced into a subject. Reg-2 unlike known Schwann cell
CC	mitogens e.g. glial growth factors/neuroglins, are upregulated during
CC	regeneration. The present sequence represents the Reg-2 protein.
XX	
SC	Sequence 175 AA;
Query Match	61.9%; Score 593; DB 20; Length 175;
Best Local Similarity	61.0%; Pred. No. 1,3e-51;
Matches 100; Conservative	30; Mismatches 34; Indels 0; Gaps 0
QY	9 MSMMILSCIIMFLSWGCEESOKLIPSRITCPDGSVAVGYCYCLLIIPOTWSNAELSCQ 68 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : MSMMILSCIIMFLSWGCEESPKRIPSRISCPGSGVAVGYCYCALFDPITWDADIELAQ 69

[illegible][illegible]

```

RESULT 6
ID AAR54098 standard; Protein; 175 AA.
XX-
AC AAR54098;
XX
DT 01-FEB-1995 (first entry)
XX
DE Mouse PAP.
XX
KW Pancreatitis-Associated Protein; PAP; mouse; human; bacteria;
KW aggregation; antibacterial; primer; PCR.
XX
OS Mus musculus.
XX
PN JP06135998-A.
XX
PD 17-MAY-1994.
XX
PF 22-OCT-1992; 92JP-0284765.
XX
PR 22-OCT-1992; 92JP-0284765.
XX
PS (SHIO) SHIONOGI & CO LTD.
XX
DR WPI; 1994-197103/24.
XX
DR N-PSDB; AA064172.
XX
PT Human and mouse pancreatitis-associated protein (PAP) - useful
PT for prepn. of proteinaceous antibacterial agent
XX
PS Claim 7-12; Page 6-7; 7pp; Japanese.
XX
CC PAP DNA has a high bacteria-aggregating activity and is useful for
CC the prepn. of PAP which can act as a proteinaceous antibacterial
CC agent. Total RNA was isolated from mouse. It was hybridised with a
CC modified salmon spermatozoa DNA and known rat PAP cDNA as a probe.
CC Two primers are given in AA064173-74.
XX
SQ Sequence 175 AA;

Query Match          59.7%; Score 572; DB 15; Length 175;
Best Local Similarity 57.6%; Pred. No. 1.7e-49;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

QY 3 PMTLCRMMSWMLLSCLMFLSWBGEESOKLPSSRITCPQGSVAYGSYCSLILIPQWMSN 62
DB 4 PMALPSVSMWMLLSCLMFLSWBGEESOKLPSSRITCPQGSVAYGSYCSLILIPQWMSN 62
QY 63 AELSCQMHFSGHLAFLLSTGEITFFVSSLVKNSLTAYQYIWMIGLHDPHSGTLPNGSGWKMS 122
DB 64 ADLACQKRPSSGNLVSLGAEBSFVSLVKSIGNSYSYWMIGLHDPHSGTLPNGSGWKMS 123
QY 123 SSNVLTFFYMERNPSTIAADRGYCAVLQSGFQKMDPNCENELPYCKF 172
DB 124 SSDVMNTFAMERNPSTISSPGHCASLSRSTAFLRKMDYCNVRLPYCKF 173

RESULT 7
ID AAR57117 standard; Protein; 175 AA.
XX
AC AAR57117;
XX
DT 21-FEB-1995 (first entry)
XX
DE Human Pancreatitis-Associated Protein.
XX
KW Human PAP; pancreatitis-associated protein; diagnosis; detection;
KW cystic fibrosis transmembrane conductance regulator; CFTR gene;
KW mucoviscidosis.
XX

```

```

OS Homo sapiens.
XX
PN W09415218-A.
XX
PD 07-JUL-1994.
XX
PF 23-DEC-1993; 93WO-FR01299.
XX
PR 24-DEC-1992; 92FR-0015730.
XX
PA (INRM) INST NAT SANTE & RECH MEDICALE.
XX
PI Dagorn J, Iovanna J, Keim V, Sarles J;
XX
DR WPI; 1994-234870/28.
XX
DR N-PSDB; AA069201.
XX
PT In vitro detection of pancreatic disease associated with CFTR
PT gene mutation - by measuring concn. of pancreatitis associated
PT protein in blood etc., suitable for neonatal diagnosis of, e.g.
XX cystic fibrosis
XX
PS Claim 1; Fig 3; 33pp; French.
XX
CC Antibodies which recognise the previously isolated and sequenced
CC human Pancreatitis-Associated protein (PAP) are claimed. They are
CC useful for measuring the amount of PAP in a sample to detect
CC pancreatic disease associated with heterozygotic mutations in the
CC CFTR gene. Such conditions result in expression of PAP at levels
CC at least 2-3 times higher than normal.
XX
SQ Sequence 175 AA;

Query Match          59.7%; Score 572; DB 15; Length 175;
Best Local Similarity 57.6%; Pred. No. 1.7e-49;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

QY 3 PMTLCRMMSWMLLSCLMFLSWBGEESOKLPSSRITCPQGSVAYGSYCSLILIPQWMSN 62
DB 4 PMALPSVSMWMLLSCLMFLSWBGEESOKLPSSRITCPQGSVAYGSYCSLILIPQWMSN 62
QY 63 AELSCQMHFSGHLAFLLSTGEITFFVSSLVKNSLTAYQYIWMIGLHDPHSGTLPNGSGWKMS 122
DB 64 ADLACQKRPSSGNLVSLGAEBSFVSLVKSIGNSYSYWMIGLHDPHSGTLPNGSGWKMS 123
QY 123 SSNVLTFFYMERNPSTIAADRGYCAVLQSGFQKMDPNCENELPYCKF 172
DB 124 SSDVMNTFAMERNPSTISSPGHCASLSRSTAFLRKMDYCNVRLPYCKF 173

RESULT 8
ID AAB43568 standard; Protein; 183 AA.
XX
AC AAB43568;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human cancer associated protein sequence SEQ ID NO:1013.
XX
KW Human: cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerable; immunomodulator;
KW antidiabetic; antiasclerotic; antirheumatic; antithrombotic; antiviral;
KW antiinflammatory; antifibrotic; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; noctropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.
XX
OS Homo sapiens.
XX

```


XX	MM000055350 -A1.
XX	PD 21-SEP-2000.
XX	PF 08-MAR-2000; 2000OWO-US05882.
XX	PR 12-MAR-1999; 99US-0124270.
XX	PA (HUMA-) HUMAN GENOME SCI INC.
XX	PI Rosen CA, Ruben SM;
XX	DR WPI; 2000-587533/55.
XX	DR N-PSDB; AAC77777.
PT	*Novel isolated nucleic acids comprising sequences encoding peptides
FT	*useful for treating or diagnosing e.g. cancer -
PS	Claim 11; Page 1593-1594; 2352pp; English.
XX	AAC77607 to AAC78448 encode the human cancer associated proteins given
CC	in AAB43398 to ABA44239. The proteins can have activities based on the
CC	tissues and cells the genes are expressed in. Example of activities
CC	include: cytostatic; proliferative; vulnerary; immunomodulator;
CC	antidiabetic; antisthmatic; antirheumatic; antiarthritic;
CC	antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC	dematological; neuroprotective; cardiant; thrombolytic; coagulant;
CC	neotropic; vasotropic; antipsoriatic and angiogenic. The
CC	polynucleotides and polypeptides can be used for preventing, treating or
CC	ameliorating medical conditions and diagnosing pathological conditions.
CC	Polyonucleotides, polypeptides, antibodies, agonists and antagonists from
CC	the present invention may be used to treat immune disorders by activating
CC	or inhibiting the proliferation, differentiation or mobilisation of
CC	immune cells, to treat disorders of haematopoietic cells, autoimmune
CC	disorders, allergic reactions, graft versus host disease and organ
CC	refection, modulate haemostatic or thrombolytic activity, modulate
CC	inflammation, cancers, cardiovascular disorders, neurological disease and
CC	bacterial or viral infections. The peptides, nucleotides, antibodies, and
CC	agonists and antagonists may be also be used in drug screens. AAC78449 to
CC	AAC78457 and ABA44240 represent sequences used in the exemplification of
CC	the present invention.
XX	
SQ	Sequence 183 AA:
Query Match	59.7%; Score 572; DB 21; Length 183;
Best Local Similarity	57.6%; Pred. No. 1.8e-49;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;	
QY	3 PMTICRMSNMLSCAMFLFVWGEESQKLPSPRTICPGGSAVAGSYCSLITIPOTWSN 62
Db	12 PMAIPLSVSMALSLCMLLSQVOGEERELPSPARKIRCPGSKRAYSGCTALFLSPSWID 71
QY	63 AEISCOMHPSSGHIAFLLTSGEITFEVSLLVKNLSITAYOIWIIGLHDSHGTLPNGSGWKMS 122
Db	72 ADLAQCKRRPSGNLVSLVGAEGSFVSLVKYSIGNSYSIWYIGLHDPTQGTPEMGEGEMS 131
QY	123 SGNVLTFYWERNRPSTADRGCAVLSQSGQXQKMDFNCENCLPRTICE 172
Db	132 SSDVMNYFWERNRPSTISSPGHCASLSRSTAFLRMWDYNCRNLPLYCKE 181
RESULT 9	
ID	AARI4795 standard; Protein; 174 AA.
K*	AARI4795;
DT	29-JAN-1992 (first entry)
DE	Fragment A3 from human pancreatitis associated protein.
KW	hpAP; pancreas; imaging; rat PSD.

OS	Homo sapiens.
PN	WO9116428-A.
PD	31-OCT-1991.
PF	18-APR-1991;
PR	20-APR-1990; 91WO-FR00323.
PA	(INRM) INSEPM INST NAT SANTE.
PI	Iovanna JL, Keim V, Dayron JC;
DR	WPI; 1991-339816/46.
NFSDB:	AAQ14619, AAQ14623.
CC	cDNA fragment of human pancreatitis associated protein -
CC	produced by genetic engineering, and the corresponding antibody,
CC	for use in the diagnosis of pancreatitis
PS	Claim 13; Page 36; 49pp; French.
SQ	The human PAP cDNA fragment S3 was cloned into pEX and the resultant recombinant transformed into E.coli. The expression product (A3) was used to generate antibodies for in vitro diagnosis of acute pancreatitis and for imaging the pancreas.
Sequence	174 AA;
Query Match	59.1%; Score 566; DB 12; Length 174;
Best Local Similarity	57.4%; Pred. No. 6.9e-49;
Matches 97; Conservative	34; Mismatches 38; Indels 0; Gaps 0;
OY	3 PMLTRMSWMILSCLMFLSWGEESOKKLPESSRTITCPOGSVAYGSCYSTLIPOTWSN 62
DB	4 PALALPVSVMILLSCIMLLSQVGEEPPRELPSARIRCPKSGAKYGSHCYALFLSPKSMWD 63
OY	63 AELSCOMHFSGLAFLLTSGEITFPVSVLYKNSLTAYQYTWGLHPBSHTLPNGSGMKWS 122
DB	64 ADLACCKRPISGNIVSYLSAEISGFVSLKSIGNSYSYWIQLHDPTQTGETPENGGEWMS 123
OY	123 SSNVLFYEWERNPSTIAADRGCAVLISOCSGFOKNDFENCENELPYICK 171
DB	124 SSDVMTYFWERNPSTISSPGHCASLSRSTAFLRKMDYCNRLPYICK 172
RESULT 10	
AAW71682	
ID	AAW71682 standard; Protein; 175 AA.
XX	AAW71682;
XX	04-DEC-1998 (first entry)
DE	Human pancreatitis-associated protein.
XX	
KW	Human pancreatitis-associated protein; PAP-2; agonist; pancreatitis;
KW	hyperplasia; hyperinsulinism; antagonist; tumour; oesophagus;
KW	intestine; metastases; Crohn's disease; ulcerative colitis;
KW	antibody; probe; PCR primer; amplification; hybridisation; inhibitor.
OS	Homo sapiens.
PN	WO9841633-A1.
PD	24-SEP-1998.
PF	20-MAR-1998; 98WO-US05699.
PR	20-MAR-1997; 97US-0822261.

PR	11-MAR-1998-	98UTS-00776512
PR	11-MAR-1998-	98UTS-00776619
PR	11-MAR-1998-	98UTS-00776649
PR	12-MAR-1998-	98UTS-00777001
PR	13-MAR-1998-	98UTS-00780704
PR	17-MAR-1998-	98UTS-00404202
PR	20-MAR-1998-	98UTS-00788860
PR	20-MAR-1998-	98UTS-00789181
PR	20-MAR-1998-	98UTS-00789366
PR	20-MAR-1998-	98UTS-00789399
PR	26-MAR-1998-	98UTS-00792564
PR	27-MAR-1998-	98UTS-00796644
PR	27-MAR-1998-	98UTS-00796654
PR	27-MAR-1998-	98UTS-00797286
PR	27-MAR-1998-	98UTS-00797286
PR	30-MAR-1998-	98UTS-00799290
PR	30-MAR-1998-	98UTS-00799293
PR	31-MAR-1998-	98UTS-00801057
PR	31-MAR-1998-	98UTS-00801165
PR	31-MAR-1998-	98UTS-00801324
PR	01-APR-1998-	98UTS-00803238
PR	01-APR-1998-	98UTS-00803349
PR	01-APR-1998-	98UTS-00803449
PR	08-APR-1998-	98UTS-00810771
PR	08-APR-1998-	98UTS-00810771
PR	09-APR-1998-	98UTS-00811195
PR	09-APR-1998-	98UTS-00812203
PR	09-APR-1998-	98UTS-00812209
PR	15-APR-1998-	98UTS-00818127
PR	15-APR-1998-	98UTS-00818388
PR	15-APR-1998-	98UTS-00819352
PR	21-APR-1998-	98UTS-00821355
PR	21-APR-1998-	98UTS-00822568
PR	22-APR-1998-	98UTS-00822569
PR	22-APR-1998-	98UTS-00822700
PR	22-APR-1998-	98UTS-00827004
PR	23-APR-1998-	98UTS-00828767
PR	23-APR-1998-	98UTS-00828767
PR	27-APR-1998-	98UTS-00832336
PR	27-APR-1998-	98UTS-00833400
PR	29-APR-1998-	98UTS-00833545
PR	29-APR-1998-	98UTS-00835354
PR	29-APR-1998-	98UTS-00835358
PR	29-APR-1998-	98UTS-00835495
PR	29-APR-1998-	98UTS-00834366
PR	29-APR-1998-	98UTS-00834369
PR	30-APR-1998-	98UTS-00843666
PR	05-MAY-1998-	98UTS-00844114
PR	06-MAY-1998-	98UTS-00844114
PR	06-MAY-1998-	98UTS-00845908
PR	07-MAY-1998-	98UTS-00845908
PR	07-MAY-1998-	98UTS-00846000
PR	07-MAY-1998-	98UTS-00846327
PR	07-MAY-1998-	98UTS-00846339
PR	07-MAY-1998-	98UTS-00846340
PR	13-MAY-1998-	98UTS-00853572
PR	15-MAY-1998-	98UTS-00853579
PR	15-MAY-1998-	98UTS-00855800
PR	15-MAY-1998-	98UTS-00855824

PR	15-MAY-1998:	98US-0085689.
PR	15-MAY-1998:	98US-0085697.
PR	15-MAY-1998:	98US-0085700.
PR	15-MAY-1998:	98US-0085704.
PR	18-MAY-1998:	98US-0086023.
PR	22-MAY-1998:	98US-0086392.
PR	22-MAY-1998:	98US-0086414.
PR	23-MAY-1998:	98US-0086430.
PR	23-MAY-1998:	98US-0086486.
PR	28-MAY-1998:	98US-0087098.
PR	28-MAY-1998:	98US-0087106.
PR	28-MAY-1998:	98US-0087208.
PR	30-JUL-1998:	98US-0094651.
PR	11-SEP-1998:	98US-0100038.
PA	(GETH) GENENTECH INC.	
XX		
PI	Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;	
XX		
DR	WPI; 1999-551358/46.	
DR	N-PSTB; AA234271.	
PT	New secreted and transmembrane polypeptides and their polynucleotides,	
PT	useful for treating blood coagulation disorders, cancers and cellular	
PT	adhesion disorders -	
XX		
PS	Claim 12: Fig 183; 530pp: English.	
XX		
CC	The present invention describes secreted and transmembrane polypeptides	
CC	and their polynucleotides. The nucleotide sequences are useful as	
CC	sources of probes, primers, for chromosome mapping, and for generation	
CC	of antisense sequences. They can also be used to create transgenic	
CC	animals. The proteins can be used to treat a variety of diseases and	
CC	disorders, depending on their function. Diseases that may be treated	
CC	include blood coagulation disorders, cancers and cellular adhesion	
CC	disorders. They may also be used to raise antibodies. AA233891 to	
CC	AA234336, and AA41685 to AA41774 represent polynucleotide and	
CC	polypeptide sequence given in the exemplification of the present	
CC	invention.	
XX		
SQ	Sequence 175 AA:	
Query Match	58.1%; Score 557; DB 20; Length 175;	
Best Local Similarity	55.6%; Pred. No. 5.6e-48;	
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps		
YY	3 PMTLCRMNWLISCLMFISVWGEESSQKRLPESRITCPQGSVANAGSYCSLLIPTQTSN 62	
DB	4 PMLIPSPSWMLLSCLTLLOVOGEETOKELDPSRISCPGSKAAGSCYALFLSPKSMMD 63	
YY	63 AELSQQHPSGHAFILFSGEITFPSSLYKNLNTATYOYIWIWGLDPHGHLPGNSGMKMS 122	
DB	64 ADLACQARRPBGKIVYSVLGABEGSFVSLVRKISINYSTIMIGLDHPDGSEPDGDWENS 123	
YY	123 SSNVLTFFMYERNPNPSTADRGYCAVALSOKSGFOKWKDNCENELPYTCERK 173	
DB	124 STDVMNFFAWEKNPSTILNPCHGCSLSRSTGFLKWKDYNCDAKLPYCCKEK 174	
RESULT 12		
AABA44311		
ID	AABA44311 standard; Protein; 175 AA.	
XX		
AC	AABA44311;	
XX		
DJ	08-FEB-2001 (first entry)	
XX		
DE	Human PRO162 (UNQ429) protein sequence SEQ ID NO:452.	
KM	Human: secreted protein; transmembrane protein; PRO; EST; cytosolic;	
KM	expressed sequence tag; detection; cancer.	
OS	Homo sapiens.	

XX PN WO200053756-A2.

XX XX 14-SEP-2000.

XX PF 18-FEB-2000; 2000WO-US04341.

XX PR 08-MAR-1999; 99WO-US05028.

PR 12-MAR-1999; 99US-0123957.

PR 29-MAR-1999; 99US-0126773.

PR 21-APR-1999; 99US-0136232.

PR 28-APR-1999; 99US-0131443.

PR 14-MAY-1999; 99US-0134287.

PR 23-JUN-1999; 99US-0141037.

PR 26-JUL-1999; 99US-0145698.

PR 29-OCT-1999; 99US-0162506.

PR 30-NOV-1999; 99WO-US28313.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.

PR 30-DEC-1999; 99WO-US31243.

PR 30-DEC-1999; 99WO-US31274.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.

PR 06-JAN-2000; 2000WO-US00376.

XX PA (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

PI Ferrara N, Flyvbjerg E, Fong S, Gao W, Geider H, Gerritsen ME;

PI Goldavski P, Gudowski PJ, Grimaldi C, Gurney AL, Hillan KJ;

PI Kildavlin LJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;

PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;

XX DR WPI: 2000-611443/58.

DR N-PSDB: AAC78569.

XX PT Novel PRO polypeptides and polynucleotides used in detection methods,

PT to target bioactive molecules to specific cells, and to modulate

PT cellular activities -

XX PS Claim 12; Fig 183; 636pp; English.

XX CC AAC78458 to AAC78599 represent polynucleotide and ESN (expressed

CC sequence tag) sequences which encode secreted or transmembrane PRO

CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic

CC activity. The polynucleotides and polypeptides can be used for detecting

CC the presence of PRO polypeptides in samples, for linking bioactive

CC molecules to cells and for modulating biological activities of cells,

CC using the polypeptides for specific targeting. The polypeptide targeting

CC can be used to kill the target cells, e.g. for the treatment of cancers.

CC The polypeptide pairs provide specific targeting of bioactive molecules

CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in

CC the isolation of the PRO polynucleotide sequences.

XX SO Sequence 175 AA:

XX

Query Match 58.1%; Score 557; DB 21; Length 175;

Best Local Similarity 55.6%; Pred. No. 5.6e-46;

Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

QY 3 PWTCIRMSWMLSCIMFLSWVEGEESQKRLPSSRTICPOGSAVAGSYCYSLILIPOTWSN 62

DB 4 PMALPSVSMMLSCILILICQVGEETQKELPPSRISCRKSGKAVGSPCYALFLSPKSWND 63

QY 63 AELSCOMFSCSHLAFLSTGEITFVSVSLKNSLTAYOTITWGLMDPSHGTLPNSSGWNKS 122

DB 64 ADIACQKRPSSCKLAVSLVSGAEFSVSLVRSISNSYITWGLMDPVOGSPPODGHENS 123

QY 123 SSVNLTFYFNERNFSLAADRGCAVLSQKSGQKMRDPCNEMLPYICRKR 173

DB 124 STDVWNTFAWEKNSITLNPCHGSLSRSTGFLAKKDDVNCACAPLYCCKR 174

RESULT 13
 AAU29235
 ID AAU29235 standard; Protein: 175 AA.
 AC AAU29235;
 NC
 DT 18-DEC-2001 (first entry)
 XX
 DE Human PRO polypeptide sequence #212.
 XX
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder
 OS Homo sapiens.
 XX
 PN WO200168848-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 28-FEB-2001; 2001WO-US06520.
 XX
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 03-MAR-2000; 2000US-187202P.
 PR 06-MAR-2000; 2000US-186968P.
 PR 14-MAR-2000; 2000US-189320P.
 PR 14-MAR-2000; 2000US-189328P.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 21-MAR-2000; 2000US-190828P.
 PR 21-MAR-2000; 2000US-191007P.
 PR 21-MAR-2000; 2000US-191048P.
 PR 21-MAR-2000; 2000US-191314P.
 PR 28-MAR-2000; 2000US-192655P.
 PR 29-MAR-2000; 2000US-193032P.
 PR 29-MAR-2000; 2000US-193053P.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 04-APR-2000; 2000US-194449P.
 PR 04-APR-2000; 2000US-194647P.
 PR 11-APR-2000; 2000US-195975P.
 PR 11-APR-2000; 2000US-196000P.
 PR 11-APR-2000; 2000US-196187P.
 PR 11-APR-2000; 2000US-196680P.
 PR 11-APR-2000; 2000US-196820P.
 PR 18-APR-2000; 2000US-198121P.
 PR 18-APR-2000; 2000US-198585P.
 PR 25-APR-2000; 2000US-199397P.
 PR 25-APR-2000; 2000US-199550P.
 PR 25-APR-2000; 2000US-199654P.
 PR 03-MAY-2000; 2000US-201516P.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14841.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 05-JUN-2000; 2000US-209832P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 22-AUG-2000; 2000US-0644848.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 XX
 PA (GENE) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AT,
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 WP1: 2001-602746/68.
 DR N-PSDB; AAS46136.
 XX
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the

Query Match	58.1%;	Score 557;	DB 23;	Length 175;
Best Local Similarity	55.68;	Pred. No. 5.6e-48;		
Matches	95;	Conservative	37;	Mismatches 39;
			Indels	0;
			Gaps	0;

Oy		3 PMICRSMWMLLSCLMFLFISVWGEGSOKKLPSSRTTQPOGSVAVGSCYCSHILIPQMNSN : : : : : : : : : :	62
Dd		4 PMAIPSYSMMLLSLCILLCQQOVBETCKELPSPRIOSCPKSAIYGSPCALFLPSKMSMD :	63
Oy		63 AELSCOMHPESGHLIAFLTSTGETTFPVSSLVKANSILTAVOIWTIGLHDPSHGTLPNSGCRKWS :: :	122
Dd		64 ADLACORRPBGKLVSALTSAGSESFVSSIIVRSINSYSYTWIGLIHDTQSSEPDDGGCWEMS :	123
Oy		123 SSNIPLFYNNERNPDSIADRGCAVLSQLSGFGFKMRDENCENELPYICKKF ::: :	173
Dd		124 STDPMNFAMFNKPSTIIINPGHCGLSRHSITGFIMKNDYNDALALPYVCXCFK :	174
	RESULT 15		
ID	ABB84876	standard; Protein; 175 AA.	
XX			
AC	ABB84876;		
DF	16-MAY-2002	(first entry)	
DE			
XX		Human PRO162 protein sequence SEQ ID NO:120.	
KW		Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerable; antiatherosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial stenosis; angina; rheumatoid arthritis; myocardial infarction; thromboembolitis; lymphangitis; tumor angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping. 	
XX		Homo sapiens.	
OS		Wo200200690-A2.	
PJ		03-JAN-2002.	
PD			
XX		20-JUN-2001; 2001WO-US19692.	
PF			
XX		23-JUN-2000; 2000US-213637P.	
PR		20-JUL-2000; 2000US-219556P.	
PR		25-JUL-2000; 2000US-220524P.	
PR		25-JUL-2000; 2000US-220664P.	
PR		28-JUL-2000; 2000WO-US20710.	
PR		02-AUG-2000; 2000US-222695P.	
PR		17-AUG-2000; 2000US-0643657.	
PR		23-AUG-2000; 2000WO-US23522.	
PR		24-AUG-2000; 2000WO-US23328.	
PR		07-SEP-2000; 2000US-230978P.	
PR		18-SEP-2000; 2000US-066410.	
PR		18-SEP-2000; 2000US-066510.	
PR		24-OCT-2000; 2000US-242922P.	
PR		08-NOV-2000; 2000WO-US30873.	
PR		10-NOV-2000; 2000WO-US30873.	
PR		01-DEC-2000; 2000WO-US32678.	
PR		20-DEC-2000; 2000US-0747259.	
PR		20-DEC-2000; 2000WO-US34956.	
PR		22-JAN-2001; 2001US-076709.	
PR		28-FEB-2001; 2001US-079649B.	
PR		28-FEB-2001; 2001WO-US06520.	
PR		01-MAR-2001; 2001WO-US06666.	
PR		09-MAR-2001; 2001US-0802706.	
PR		14-MAR-2001; 2001US-0808689.	
PR		22-MAR-2001; 2001US-0816744.	
PR		05-APR-2001; 2001US-0828366.	
PR		10-MAY-2001; 2001US-0854208.	
PR		10-MAY-2001; 2001US-0854280.	
PR		23-MAY-2001; 2001US-086628.	
PR		25-MAY-2001; 2001US-0866034.	
PR		25-MAY-2001; 2001WO-US17092.	

A:Note: only Intron/exon boundaries are shown; exon I and the beginning of exon II are
encompassed of the open reading frame to an AUG codon in exon I is shown in accession A59313
R:Ussetti, N.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
submitted to Genbank, August 1993
A:Reference number: A59313
A:Accession: A59313
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: MMARV',1-175 <DUS>
A:Cross-references: GB:U07127; NID:g349550; PIDD:AAA41805.1; PID:g349551
A:Note: an incorrect initiation codon was used
R:Iovanna, J.L.; Keim, V.; Bosshard, A.; Orelle, B.; Frigerio, J.M.; Dusetti, N.; Dagorn
Am. J. Physiol. 265, G611-G618, 1993
A:Title: PAP, a pancreatic secretory protein induced during acute pancreatitis, is expressed
A:Reference number: I51899; MUID:94056762; PMID:8238345
A:Accession: I51899
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-175 <IOV>
A:Cross-references: GB:M8049; NID:g393210; PIDD:AAA16341.1; PID:g393211
A:Note: in Genbank entry RAMPAC, release 113.0, the source is designated as Rattus rattus
R:Kamimura, T.; West, C.; Beutler, E.
Gene 118, 299-300, 1992
A:Title: Sequence of a cDNA clone encoding a rat Reg-2 protein.
A:Reference number: JCI257; MUID:92380521; PMID:1511905
A:Accession: JCI257
A:Molecule type: mRNA
A:Residues: 1-6, 'S', 8-175 <RAM>
A:Cross-references: GB:543715; NID:g254694; PIDD:RAMB3103.1; PID:g254695
R:Iovanna, J.; Orelle, B.; Keim, V.; Dagorn, J.C.
J. Biol. Chem. 266, 24664-24669, 1991
A:Title: Messenger RNA sequence and expression of rat pancreatitis-associated protein, a
A:Reference number: A41719; MUID:92105133; PMID:1722211
A:Accession: A41719
A:Molecule type: mRNA
A:Residues: 1-175 <IOV2>
A:Cross-references: GB:M5149; NID:g206030; PIDD:AAA41807.1; PID:g206031
A:Note: the amino-terminal residue of the mature protein was identified as Glu
C:Genetics:
A:Gene: pap
A:Introns: 26/1; 65/3; 111/3; 154/1
A:Note: the first intron occurs before the initiator codon
C:Superfamily: tetranectin; C-type lectin homology
C:Keywords: lectin; pancreas
F:1-26/Domain: signal sequence #status predicted <SIG>
F:27-175/Product: pancreatitis-associated protein #status experimental <MAT>
F:40-171/Domain: C-type lectin homology <LCH>
F:40-51,68-171,146-163/Disulfide bonds: #status predicted

Query Match	61.9%	Score 593;	DB 2;	Length 175;
Best Local Similarity	61.0%	Pred. No. 3.9e-47;		
Matches 100;	Conservative 30;	Mismatches 34;	Indels 0;	Gaps 0;
Db	9	MSWMLSCIMPLSWEGESQKIPSPSRITCPQGSVAVGSCYCSLLILPQWMAELSCQ	68	
Qy	-	MSWMLSCIMPLSWEGESQKIPSPSRITCPQGSVAVGSCYCSLLILPQWMAELSCQ	68	
Db	10	MSWMLSCIMPLSWEGESQKIPSPSRITCPQGSVAVGSCYCSLLILPQWMAELSCQ	69	
Qy	69	MHSCHLAFLLSTGCTITVSSILYKNSLTAQYIWIGLDPSHGTLIPNCSGKMWSSNYLT	128	
Db	70	KRPBSHLVSVLVAASPLASVKNKNGNSIOTYTWIGLHDPYLGGEPPGGGWMNSNDIMN	129	
Qy	129	FYNWERNPSIAADRCYCAVLISQSGCFQKWRDFNCENELPYICKF	172	
Db	130	FYNWERNPSIAADRCYCAVLISQSGCFQKWRDFNCENELPYICKF	173	

RESULT 3
A49616
pancreatitis-associated protein precursor - human
N:Alternate names: C-type lectin; pancreatic stone protein homolog HIP
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jul-2000
C:Accession: A49616; A44931; S29821; S48197; I55580

	RiDusettl, N.J.; Frijerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C.; Iovanna, J.L.
	Genomics 19; 108-114; 1994
	A>Title: Molecular cloning, genomic organization, and chromosomal localization of the
	A:Reference number: A49616; MUID:94245143; PMID:8188210
	A:Accession: A49616
	A:Molecule type: DNA
	A:Residues: 1-175 <DDSS>
	A:Cross-references: GB:I15533; NID:g482908; PIDN:AAA60020.1; PID:g482909
	Rilasserre, C.; Christa, L.; Simon, M.T.; Vernier, P.; Brechot, C.
	Cancer Res. 52; 5089-5095; 1992
	A>Title: A novel gene (HIP) activated in human primary liver cancer.
	A:Reference number: A44931; MUID:92386513; PMID:1325291
	A:Accession: A44931
	A:Molecule type: mRNA
	A:Residues: 1-175 <LASS>
	A:Cross-references: GB:X68641; NID:g312806; PIDN:CAA4605.1; PID:g312807
	A:Experimental source: hepatocellular carcinoma
	A>Note: Sequence extracted from NCBI backbone (NCBIN:113007, NCBIN:113008)
	R:Ittoh, T.; Teraoka, H.
	Biochim. Biophys. Acta 1172; 184-186; 1993
	A>Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homo
	A:Reference number: S29821; MUID:93176807; PMID:7679928
	A:Accession: S29821
	A>Status: preliminary
	A:Molecule type: mRNA
	A:Residues: 1-175 <ITOO>
	A:Cross-references: GB:D13510; NID:g285970; PIDN:BAA02728.1; PID:g285971
	Rilasserre, C.; Simon, M.T.; Ishikawa, H.; Diriong, S.; Nguyen, V.C.; Christa, L.; Ve
	Eur. J. Biochem. 224; 29-38; 1994
	A>Title: Structural organization and chromosomal localization of a human gene (HIP/PA
	A:Reference number: S48197; MUID:94357229; PMID:8076648
	A:Accession: S48197
	A>Status: preliminary
	A:Molecule type: DNA
	A:Residues: 1-175 <LA2>
	R:Orelle, B.; Klein, V.; Masciotra, L.; Dagorn, J.C.; Iovanna, J.L.
	J. Clin. Invest. 90; 2284-2291; 1992
	A>Title: Human pancreaticitis-associated protein. Messenger RNA cloning and expression
	A:Reference number: I55580; MUID:93107309; PMID:1469087
	A:Accession: I55580
	A>Status: preliminary; translated from GB/EMBL/DDBJ
	A:Molecule type: mRNA
	A:Residues: 1-175 <RBS>
	A:Cross-references: GB:S51768; NID:g262368; PIDN:AAB24642.1; PID:g262369
	C:Genetics:
	A:Gene: GDB:PAP; HIP
	A:Cross-references: GDB:136839; OMIM:167805
	A:Map position: 2p12-2p12
	A:Introns: 26/1; 65/3; 111/3; 154/1
	C:Keywords: acute phase; extracellular protein; pancreas
	F:1-26/Domain: signal sequence #status predicted <SIG>
	F:27-175/Product: pancreaticitis-associated protein #status predicted <MAT>
	F:40-51,68-171,146-163/disulfide bonds: #status predicted
Query Match	59.7%; Score 572; DB 2; Length 175;
Best local similarity	57.6%; Pred. No. 3; de-45;
Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;	
OY	3 PMTLCRMGSMMLLSCLMPLISWGEESQKRLPSSRTCPQGSAVAGSYCYSLILIPOTWSN 62
	: : : : : :
DB	4 PALPSYSVMLLSCLMLISVOYGEEPRQLRSARIRPKSGAKAVSHCYALFLSPKSWTD 63
OY	63 AELSCQMHPFSGHIALLTSTGETPVSSLVKNSLRATAYOIYWGLNDPSHGILPNNSGKWS 122
	:: :: : : : : : :
DB	64 ADLAQCQRKPSCGLSVLSLGAGSFVSSLYTKSIGNSYSVYWGHLDPPTQGEENEGEWS 123
OY	123 SSNVTLTFNNERNPISIADRCGCAVLISQSGFOKMRDFCENEPIPYCKF 172
	:: : : : : : :
DB	124 SSDVNWNYFAWRNPSTISSPGHCASLSRSTAFLEMKDYINCMVRLLPYCKF 173

RESULT 4

A37194

pancreatic thread protein precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 20-Aug-1999

C:Accession: A37194; A53897

R:de la Monte, S.M.; Ozuturk, M.; Wands, J.R.

J. Clin. Invest. 86, 1004-1013, 1990

A:Title: Enhanced expression of an exocrine pancreatic protein in Alzheimer's disease and

A:Reference number: A37194; MUID:90368981; PMID:2394826

A:Accession: A37194

A:Molecule type: mRNA

A:Residues: 1-175

A:Cross-references: GB:M59794; NID:g163648; PIDN:AAA30750.1; PID:g163649

R:Cal, L.; Harris, W.R.; Marshak, D.R.; Gross, J.; Crabbs, J.W.

J. Protein Chem. 9, 623-632, 1990

A:Title: Structural analysis of bovine pancreatic thread protein.

A:Reference number: A53897; MUID:91197388; PMID:2085387

A:Accession: A53897

A:Molecule type: protein

A:Residues: 38-138;141-175 <CA1>

C:Comment: The purified protein undergoes a reversible globule-fibril transformation and

C:Superfamily: tetranectin; C-type lectin homology

C:Keywords: disulfide bond; extracellular protein; pancreas

F:40-170/Product: pancreatic thread protein chain A #status experimental <ACH>

F:141-175/Product: pancreatic thread protein chain B #status experimental <BCH>

Query Match

Best Local Similarity 55.5%; Score 531.5; DB 2; Length 175;

Matches 94; Conservative 32; Mismatches 46; Indels 1; Gaps 1;

QY 1 MUP-MTLCMSMMLSCMLFSLWVGEESOKKLPSSRTTCPOGSVAVGSCYSLILIPOT 59

DB 1 MUPSLGLPRISWMLSCMLLSQIOGENSOKEPBARISCSCGSMAYRSHCYALFKPKPT 60

QY 60 WSNALSCOMHPSGHLAFLSTGETTFVSVLVKNSLRYOYIWIIGLHDPHSGTLPNCSGW 119

DB 61 WMDADLACQKRPSGHLVSLSGAESFVASILVRNMLNQGSDIWLHDPHTGSEANAGW 120

QY 120 KSSSNVLTFFYWMERNPSTIAADRGYCAVLSCGSGQKRDNCENELPYICKK 172

DB 121 EWSNDVLYNVMETDPAISPGYCSLSRSSGTLKMRDHNCMLNLPYCKF 173

RESULT 5

S54979

pancreatitis-associated protein PAP-3 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 20-Aug-1999

C:Accession: S54979; S43438

R:Dusetli, N.J.; Frigerio, J.M.; Szpirer, C.; Dagorn, J.C.; Iovanna, J.L.

Biochem. J. 307, 9-16, 1995

A:Title: Cloning, expression and chromosomal localization of the rat pancreatitis-associ-

A:Reference number: S54979; MUID:95234061; PMID:7717998

A:Accession: S54979

A:Molecule type: DNA

A:Residues: 1-174 <DUS>

A:Cross-references: EMBL:U09193; NID:g483931; PIDN:AAA79231.1; PID:g483932

R:Frigerio, J.M.; Dusetli, N.J.; Garrido, P.; Dagorn, J.C.; Iovanna, J.L.

Biochim. Biophys. Acta 1216, 329-331, 1993

A:Title: The pancreatitis associated protein III (PAP III), a new member of the PAP gene

A:Reference number: S43438; MUID:94060113; PMID:8241280

A:Accession: S43438

A:Molecule type: mRNA

A:Residues: 1-174 <FRI>

A:Cross-references: GB:L20869; GB:S67496; NID:g463279; PIDN:AAA41809.1; PID:g463280

C:Genetics: 26/1; 65/3; 111/3; 153/1

A:Superfamily: tetranectin; C-type lectin homology

F:40-170/Domain: C-type lectin homology <LCH>

Query Match 54.1%; Score 518; DB 2; Length 174;

Best Local Similarity 52.9%; Pred. No. 2.9e-40;

Matches 92; Conservative 39; Mismatches 41; Indels 2; Gaps 2;

QY 1 MUP-MTLCMSMMLSCMLFSLWVGEESOKKLPSSRTTCPOGSVAVGSCYSLILIPOT 59

DB 1 MUPSLGLPRISWMLSCMLLSQIOGENSOKEPBARISCSCGSMAYRSHCYALFKPKPT 60

QY 60 WSNALSCOMHPSGHLAFLSTGETTFVSVLVKNSLRYOYIWIIGLHDPHSGTLPNCSGW 119

DB 61 WMDADLACQKRPSGHLVSLSGAESFVASILVRNMLNQGSDIWLHDPHTGSEANAGW 120

QY 120 KSSSNVLTFFYWMERNPSTIAADRGYCAVLSCGSGQKRDNCENELPYICKK 173

DB 121 EWSNDVLYNVMETDPAISPGYCSLSRSSGTLKMRDHNCMLNLPYCKF 173

RESULT 6

I83377

regenerating protein III (reg III) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 20-Aug-1999

C:Accession: I60296; I83377

R:Suzuki, Y.; Yonekura, H.; Watanabe, T.; Unno, M.; Morizumi, S.; Miyashita, H.; Oka

Gene 144, 315-316, 1994

A:Title: Structure and expression of a novel rat RegIII gene.

A:Reference number: I60296; MUID:94314238; PMID:8039722

A:Accession: I60296

A:Molecule type: mRNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D23676; NID:g471157; PIDN:BA04904.1; PID:g471158

A:Accession: I83377

A:Molecule type: protein

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Accession: I83377

A:Molecule type: DNA

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Accession: I83377

A:Molecule type: protein

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Accession: I83377

A:Molecule type: protein

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Accession: I83377

A:Molecule type: protein

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Accession: I83377

A:Molecule type: protein

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Accession: I83377

A:Molecule type: protein

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Accession: I83377

A:Molecule type: protein

A:Residues: 1-174 <RES>

A:Cross-references: GB:D26078; NID:g471159; PIDN:BA05071.1; PID:g471160

A:Accession: I83377

A:Molecule type: protein

A:Residues: 1-174 <RES>

Wed Apr 16 12:14:49 2003

us-08-401-530-2.rpr

Page 7

```

Oy 76 APLLSGELTPVSSLYVKNLSLTAQYQIMIGLHPDSGTLIPNDSGKMSNVLFYFMYER 134
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 VSIESSEGDPAFHLIAQKIKSAKIHVIMILRPNQK---EKQSTIENSDDGSLEYEW-- 117
Oy 135 NPSTADRGCAVLSQSGSPQKMPDCEGELPYYICK 171
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 ---IEESKKCLGAVHIEGFHKMEVFCBEODPFVCE 151
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```
Search completed: April 16, 2003, 10:47:46
Job time : 18 secs
```



```

DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Signal; Lectin.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 175 PANCREATIC BETA CELL GROWTH FACTOR.
FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19940 MW; 3854F36BA35D17CE CRC64;

Query Match 100.0%; Score 958; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 7.8e-76;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLEPMLCRMSNMWLSCLMFLSWVEGESQKRLPSRITCPQGSVAYGSCYSLIIPQTW 60
DB 2 MLEPMLCRMSNMWLSCLMFLSWVEGESQKRLPSRITCPQGSVAYGSCYSLIIPQTW 61
OY 61 SNAELSCQMHPFSGHIAFLITSGEITFVSLYKNSLTAYQYIWIIGHDPSHGTLPGSGWK 120
DB 62 SNAELSCQMHPFSGHIAFLITSGEITFVSLYKNSLTAYQYIWIIGHDPSHGTLPGSGWK 121
OY 121 WSSSNVLTFFYNNERNPSTADRGCAVLSQKSGFQKMRDENCENELPYICKFKV 174
DB 122 WSSSNVLTFFYNNERNPSTADRGCAVLSQKSGFQKMRDENCENELPYICKFKV 175

RESULT 2
PAP1_MOUSE STANDARD; PRT; 175 AA.
AC P35230;
ID PAP1_MOUSE
DR 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (REG III-beta).
DE PAPI OR PAP OR REG3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas, and small intestine;
RX MEDLINE=93176807; PubMed=7679928;
RA Itoh T., Terakawa H.;
RT "Cloning and tissue-specific expression of cDNAs for the human and
RT mouse homologues of rat pancreatitis-associated protein (PAP).";
RL Biochim. Biophys. Acta 1172:184-186(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=97208868; PubMed=9055810;
RA Narushima Y., Uno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.;
RT "Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
RL Gene 185:159-168(1997).
RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-39.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreas;
RX MEDLINE=92105133; PubMed=1722211;
RA Iovanna J., Orelle B., Keim V., Dagnon J.-C.;
RT "Messenger RNA sequence and expression of rat pancreatitis-associated
RT protein, a lectin-related protein overexpressed during acute
RT experimental pancreatitis.";
RL J. Biol. Chem. 266:24664-24669(1991).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=9405762; PubMed=8238345;
RA Iovanna J.L., Keim V., Bosshard A., Orelle B., Frigerio J.M.,
RA Dusetti N., Dagnon J.C.;

```

```

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D13509; BAA02727.1; -
DR EMBL; D63359; BAA18928.1; -
DR EMBL; D63360; BAA18929.1; -
DR PIR; S29822; S29822.
DR HSSP; P05451; ILIT.
DR MGD; MGI:97478; Pap.
DR InterPro; IPR001304; Lectin_C.
DR InterPro; IPR003990; Pancreatis_ac.
DR Pfam; PF00059; lectin.c1.
DR PRINTS; PR01504; PNCREATITISAP.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Signal; Lectin; Inflammatory response; Acute phase; Multigene family.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 1.
FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19476 MW; 44B3101171E79775 CRC64;

Query Match 63.2%; Score 605.5; DB 1; Length 175;
Best Local Similarity 60.7%; Pred. No. 1.7e-45;
Matches 105; Conservative 29; Mismatches 36; Indels 1; Gaps 1;

OY 1 MLEPMLCR-MSNMWLSCLMFLSWVEGESQKRLPSRITCPQGSVAYGSCYSLIIPQT 59
DB 1 MLEPMLCRMSNMWLSCLMFLSWVEGESQKRLPSRITCPQGSVAYGSCYSLIIPQT 60
OY 60 WSNELSCQMHPFSGHIAFLITSGEITFVSLYKNSLTAYQYIWIIGHDPSHGTLPGSGWK 119
DB 61 WSNELSCQMHPFSGHIAFLITSGEITFVSLYKNSLTAYQYIWIIGHDPSHGTLPGSGWK 120
OY 120 WSSSNVLTFFYNNERNPSTADRGCAVLSQKSGFQKMRDENCENELPYICKFKV 172
DB 121 WSSSNVLTFFYNNERNPSTADRGCAVLSQKSGFQKMRDENCENELPYICKFKV 173

RESULT 3
PAP1_RAT STANDARD; PRT; 175 AA.
ID PAP1_RAT
DR 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (Peptide 23) (REG-2).
DE PAPI OR PAP OR REG2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-39.
RC STRAIN=Sprague-Dawley; TISSUE=Pancreas;
RX MEDLINE=92105133; PubMed=1722211;
RA Iovanna J., Orelle B., Keim V., Dagnon J.-C.;
RT "Messenger RNA sequence and expression of rat pancreatitis-associated
RT protein, a lectin-related protein overexpressed during acute
RT experimental pancreatitis.";
RL J. Biol. Chem. 266:24664-24669(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=9405762; PubMed=8238345;
RA Iovanna J.L., Keim V., Bosshard A., Orelle B., Frigerio J.M.,
RA Dusetti N., Dagnon J.C.;

```


RT PAP, a pancreatic secretory protein induced during acute
 RT pancreatitis, is expressed in rat intestine.;
 RL Am. J. Physiol. 265:G611-G618(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Mistral; TISSUE-Liver;
 RX MEDLINE-93300847; PubMed-8314803;
 RA Dusetti N.J., Frigerio J.M., Kelm V., Dagorn J.C., Iovanna J.;
 RT "Structural organization of the gene encoding the rat pancreatitis-
 RT associated protein. Analysis of its evolutionary history reveals an
 RT ancient divergence from the other carbohydrate-recognition domain-
 RT containing genes.";
 RL J. Biol. Chem. 268:14470-14475(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-92380521; PubMed-1511905;
 RA Yamamura T., West C., Reutler E.;
 RT "Sequence of a cDNA clone encoding a rat Reg-2 protein.";
 RL Gene 118:299-300(1992).
 RN [5]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-Sprague-Dawley; TISSUE-Pituitary;
 RX MEDLINE-95203187; PubMed-7895644;
 RA Katumata N., Chakraborty C., Myal Y., Schroedter I.C.,
 RT Murphy L.J., Shu R.P., Friesen H.G.;
 RT "Molecular cloning and expression of peptide 23, a growth hormone-
 RT releasing hormone-inducible pituitary protein.";
 RL Endocrinology 136:1332-1339(1995).
 CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
 CC BACTERIAL PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
 CC PANCREATIC ACINAR CELLS.
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN INTESTINE.
 CC -1- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF
 CC PANCREATIC INFLAMMATION. SECRETED ALSO BY PITUITARY CELLS; THE
 CC SECRETION THERE IS STIMULATED BY GH-RELEASING HORMONE AND
 CC INHIBITED BY SOMATOSTATIN.
 CC -1- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M55149; AAA1807.1; -;
 DR EMBL: M98049; AAA16341.1; -;
 DR EMBL: L07127; AAA1805.1; ALT_INIT.
 DR EMBL: S43715; AAB23103.1; -;
 DR EMBL: S77413; AAB33848.2; -;
 DR PIR: A41719; A41719.
 DR HSSP: P05451; 10DD.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR003990; Pancreatis-ac.
 DR Pfam: PF00059; lectin_c.1.
 DR PRINTS: PR01504; PNCREATITAP.
 DR SMART: SM00034; CLECT. 1.
 DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
 DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
 KW Signal; Lectin; Inflammatory response; Acute phase.
 FT SIGNAL 1 26
 FT CHAIN 27 175 PANCREATITIS-ASSOCIATED PROTEIN 1.
 FT* DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 40 51 BY SIMILARITY.
 FT DISULFID 68 171 BY SIMILARITY.
 FT DISULFID 146 163 BY SIMILARITY.
 FT CONFLICT 7 163 F->S (IN REF. 4).
 FT CONFLICT 123 123 S->T (IN REF. 5).
 SQ SEQUENCE 175 AA; 19617 MW; C43892BF31B0B525 CRC64;

Query Match 61.9%; Score 593; DB 1; Length 175;
 Best Local Similarity 61.0%; Pred. No. 2,1e-44;
 Matches 100; Conservative 30; Mismatches 34; Indels 0; Gaps 0;
 Oy 9 MSWMLSCIMFLSWESEESQKPLPSRITPCGSAVAGSYCYSLLLIPQWNAELSCQ 68
 Db 10 MSWMLSCIMFLSVOGEDSPKPIPSARISCPKSGAVSYCYALFQIPQTFDAELACQ 69
 Oy 69 MRSGLAFLSTGEITFVSGLYKNSLITAYQYTWICLHPSPGTLPNSGKWKSSNVLT 128
 Db 70 KRPGHLVSYLVNAEASFSLAMKNGNSYQYTWICLHPDPLGEPNGGGMWMSNNDIMN 129
 Oy 129 FYNERNPSIADRGYCAVLQSKSGFGKMRDFNCENELPYCKF 172
 Db 130 YVNERNPSTALDRGFCGSLSRSSGFLRMWDTCVRLPYCKF 173
 RESULT 4
 PAPI_HUMAN STANDARD; PRT; 175 AA.
 AC 006141;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Pancreatitis-associated protein 1 precursor.
 GN PAPI OR PAPI OR HIP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Pancreas; and Small intestine;
 RX MEDLINE-93176807; PubMed-7679928;
 RA Itoh T., Teroka H.;
 RT "Cloning and tissue-specific expression of cDNAs for the human and
 RT mouse homologues of rat pancreatitis-associated protein (PAP).";
 RL Biochim. Biophys. Acta 1172:184-186(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Pancreas;
 RX MEDLINE-93107309; PubMed-1469087;
 RA Orelle B., Kelm V., Masciotra L., Dagorn J.-C., Iovanna J.-L.;
 RT "Human pancreatitis-associated protein. Messenger RNA cloning and
 RT expression in pancreatic diseases.";
 RL J. Clin. Invest. 90:2284-2291(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RX MEDLINE-92386513; PubMed-1325291;
 RA Lasserre C., Christa L., Simon M.T., Vernier P., Brechot C.;
 RT "A novel gene (HIP) activated in human primary liver cancer.";
 RL Cancer Res. 52:5089-5095(1992).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Blood;
 RX MEDLINE-94245143; PubMed-8188210;
 RA Dusetti N.J., Frigerio J.M., Fox M.F., Swallow D.M., Dagorn J.C.,
 RT Iovanna J.L.;
 RT "Molecular cloning, genomic organization, and chromosomal
 RT localization of the human pancreatitis-associated protein (PAP)
 RT gene.";
 RL Genomics 19:108-114(1994).
 CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
 CC BACTERIAL PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
 CC PANCREATIC ACINAR CELLS.
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN INTESTINE. LOW
 CC EXPRESSION IS FOUND IN HEALTHY PANCREAS.
 CC -1- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF
 CC PANCREATIC INFLAMMATION.
 CC -1- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS AND
 CC IN SOME PATIENTS WITH CHRONIC PANCREATITIS.

CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: D13510; BA02728.1; -
 DR EMBL: M84337; AAA36415.1; -
 DR EMBL: S51768; AAB24642.1; -
 DR EMBL: X68641; CAA48605.1; -
 DR EMBL: L15533; AAA60020.1; -
 DR PIR: A44931; A44931.
 DR PIR: S29821; S29821.
 DR HSSP: P05451; 10DD.
 DR Genew: HGNC:8601; PAP.
 DR MIM: 167805; -
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; Lectin_C.1.
 DR PRINTS: PR01504; PNCREATITAP.
 DR SMART: SM00034; CLECT.1.
 DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
 DR Signal: Lectin; Inflammatory response; Acute phase.
 KM SIGNAL 1 26
 FT CHAIN 1 26 PANCREATITIS-ASSOCIATED PROTEIN 1.
 FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 40 51 BY SIMILARITY.
 FT DISULFID 68 171 BY SIMILARITY.
 FT DISULFID 146 163 BY SIMILARITY.
 FT CONFLICT 173 175 FTD -> VH (IN REF. 2).
 SQ SEQUENCE 175 AA; 19395 MW; C51149PAC22EB68C CRC64;

Query Match 59.7%; Score 572; DB 1; Length 175;
 Best Local Similarity 57.6%; Pred. No. 1.3e-42;
 Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

OY 3 PNTICRSMWMLSCMLFSLWVEGESOKLPSSRTCPGSGVAVGYCYCLILIPOTSMN 62
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 DB 4 PAHLSVSMMLSCMLLSQVGEPRQRLPSARIRCPGSAVYSKCYALFLSKRMTD 63
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 OY 63 AELSCQMFSGHLAFLSTGELTFVSSIVKNSLTAYQYTWIGLHDPESHGTLPNGSGKMS 122
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 DB 64 ADIACQKRSPGSHLAVSLVSGAESEFVSILVKSIGNSYSYWIIGLHDPGTGTEPNGESEMS 123
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 OY 123 SSNVLFYFWNERNPSTIADRGYCAVLSQKSGFQKMRDNCENELPYCKF 172
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 DB 124 SSDVMYFWNERNPSTIISPGHCAISLRSATFLRKNDVNCVRLPYCKF 173
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 RESULT 5

LITH_BOVIN STANDARD; PRT; 175 AA.
 AC P23132;
 DT 01-NOV-1991 (Rel. 20. Created)
 DT 01-NOV-1991 (Rel. 20. Last sequence update)
 DT 15-JUN-2002 (Rel. 41. Last annotation update)
 DE Lithostathine precursor (Pancreatic stone protein) (PSP) (Pancreatic
 DE thread protein) (PTP) (Islet of Langerhans regenerating protein) (REG)
 DE (Islet cells regeneration factor) (ICRF).
 GN PTP.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90368981; PubMed=2394826;

RA de la Monte S.M., Ozturk M., Wands J.R.;
 RT "Enhanced expression of an exocrine pancreatic protein in Alzheimer's
 RT disease and the developing human brain";
 RL J. Clin. Invest. 86:1004-1013(1990).
 RN [2]
 RP SEQUENCE OF 38-138 AND 141-175.
 RX MEDLINE=91197388; PubMed=2085387;
 RA Cal L., Harris W.R., Marshak D.R., Gross J., Grab J.W.;
 RT "Structural analysis of bovine pancreatic thread protein.";
 RL J. Protein Chem. 9:623-632(1990).
 RN [3]
 RP SEQUENCE OF 38-85 AND 141-175.
 RX MEDLINE=85298214; PubMed=3862086;
 RA Gross J., Brauer A.W., Brinkhurst R.F., Corbett C., Margolies M.N.;
 RT "An unusual bovine pancreatic protein exhibiting pH-dependent
 RT globule-fibril transformation and unique amino acid sequence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5627-5631(1985).
 CC -1- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM
 CC CARBONATE PRECIPITATION.
 CC -1- SUBUNIT: CLEAVED TO GIVE AN A CHAIN AND A B CHAIN JOINED BY A
 CC DISULFIDE BOND.
 CC -1- TISSUE SPECIFICITY: IN PANCREATIC ACINAR CELLS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: M59794; AAA30750.1; -
 DR PIR: A37194; A37194.
 DR HSSP: P05451; 10DD.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR003990; Pancreatis-ac.
 DR Pfam: PF00059; Lectin_C.1.
 DR PRINTS: PR01504; PNCREATITAP.
 DR SMART: SM00034; CLECT.1.
 DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
 DR Glycoprotein: signal, Lectin.
 KM SIGNAL 1 26
 FT PROPEP 27 37
 FT CHAIN 38 175 POTENTIAL.
 FT CHAIN 38 138 LITHOSTATHINE.
 FT CHAIN 141 175 A CHAIN.
 FT DOMAIN 38 173 B CHAIN.
 FT DISULFID 40 51 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 68 171 BY SIMILARITY.
 FT DISULFID 146 163 BY SIMILARITY.
 FT CONFLICT 84 85 EE -> FF (IN REF. 3).
 SQ SEQUENCE 175 AA; 19334 MW; C270E70B7E91D6A CRC64;

Query Match 55.5%; Score 531.5; DB 1; Length 175;
 Best Local Similarity 54.3%; Pred. No. 4.1e-39;
 Matches 94; Conservative 32; Mismatches 46; Indels 1; Gaps 1;

OY 1 MLP-MTLCRSMWMLSCMLFSLWVEGESOKLPSSRTCPGSGVAVGYCYCLILIPOT 59
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 DB 1 MLPISGIPRSMMLSCMLLSQVGEPRQRLPSARIRCPGSAVYSKCYALFLFTPTK 60
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 OY 60 WSNELSCQMFSGHLAFLSTGELTFVSSIVKNSLTAYQYTWIGLHDPESHGTLPNGSGM 119
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 DB 61 WMDADNACQKRSPGSHLAVSLVSGAESEFVSILVKSIGNSYSYWIIGLHDPGTGTEPN 120
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 OY 120 KWSSNVLFYFWNERNPSTIADRGYCAVLSQKSGFQKMRDNCENELPYCKF 172
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 DB 121 EWSNDVLYFWNERNPSTIISPGHCAISLRSRSGYLKWRDNCNMLPYCKF 173
 || : ||||| ||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
 RESULT 6

Db 121 EBNSDVLAATVLMWDDGPSTVNRHGCGSLTASSGFLKMGDYCDGLTFPCNRK 174

RESULT 7

ID	PAP3_MOUSE	STANDARD:	PRT:	174 AA.
AC	009049;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Pancreaticitis-associated protein 3 precursor (REG III-gamma).			
GN	PAP3 OR REG3G.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-C37BL/6J; TISSUE-Liver and Pancreas;			
RA	MEDLINE-9720868; PubMed-9055810;			
RA	Narushtina Y., Uno M., Nakagawa K.-I., Mori M., Miyashta H.,			
RA	Suzuki Y., Noguchi N., Takasawa S., Kunagai T., Yonekura H.,			
RA	Okamoto H.;			
RT	"structure, chromosomal localization and expression of mouse genes			
RT	encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";			
RL	Gene 185:159-168(1997).			
CC	- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF			
CC	BACTERIAL PROLIFERATION.			
CC	- SUBCELLULAR LOCATION: Secreted.			
CC	- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN THE SMALL			
CC	INTESTINE, MODERATELY IN COLON AND AT AN EXTREMELY LOW LEVEL IN			
CC	HEALTHY PANCREAS.			
CC	- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed, usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL: D63361; BAA18930.1; -			
DR	EMBL: D63362; BAA18931.1; -			
DR	HSSP: P05451; ILIT.			
DR	MCD: MG1:109406; Reg3g.			
DR	InterPro: IPR001304; Lectin_C.			
DR	InterPro: IPR003990; Pancreatis.ac.			
DR	Pfam: PF00059; lectin_c.1.			
DR	PRINTS: PR01504; PNCREATITSAF.			
DR	SMART: SM00034; CLEC7.1.			
DR	PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NRG.			
DR	PROSITE: PS00611; C-TYPE_LECTIN_2.1.			
FT	Signal: Lectin; Inflammatory response; Acute phase; Multigene family.			
FT	CHAIN 1 26 POTENTIAL.			
FT	DOMAIN 27 174 PANCREATITIS-ASSOCIATED PROTEIN 3.			
FT	DISULEID 38 172 C-TYPE LECTIN (LONG FORM).			
FT	DISULEID 40 51 BY SIMILARITY.			
FT	DISULEID 68 170 BY SIMILARITY.			
FT	DISULEID 145 162 BY SIMILARITY.			
SO	SEQUENCE 174 AA; 19307 MW; 5575E9E36A4D8CF CRC64;			

Query Match 54.1%; Score 518; DB 1; Length 174;

Best local Similarity 53.4%; Pred. No; 5.9e-38;

Matches 93; Conservative 35; Mismatches 44; Indels 2; Gaps 2;

1 MLP-METCRSMALLSCLEMFISWVEGESEOKKLPSSRTTCOGSVAAGSYSLIIPOT 59

1 MPRITITIMSMALLSCLMLISOVQEPVAKADAPSSRSCSKGRALGICVAFPSYSKN 60

60 WSNALSCQMHPSGRIAPLITSTGEITFVSSLYKNSLTAIVYTIWIGLHDPHGTLPMNGSM 119

61 WYADAAACCKRPBGIVSVTLSGAENSFLSMKSGNSGVYVWIGLHDPGLGPEPNRGM 120

```

07      120 KWSSNVLTEFWNRBNPISADRGCAVLSQKSGFQWRCBNCENLPHYCKFK 173
           :::::~::~||| ||| :::: ~:|||| | ||| : | |||:::|||
Db       121 EWSNDAVLTFYFNWRNPISADRGCAVLSQKSGFLKNREYNCHLELPYCCKFK 173
                                           -----
RESULT 8
PAP3_RAT
ID   PAP3_RAT              STANDARD;          PRT;         174 AA.
AC   P42654;               01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DR   DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE   Pancreatitis-associated protein 3 precursor.
GN   PAP3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Intestine;
RA   MEDLINE=94060113; PubMed=8241280;
RT   Frigerio J.-M., Dusetell N.J., Garrido F., Dagorn J.C., Iovanna J.L.;
RL   "the pancreatitis associated protein III (PAP III), a new member of
    the PAP gene family."
    Biochim. Biophys. Acta 1216:329-331(1993).
CC   -! FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
        BACTERIAL PROLIFERATION.
CC   -! SUBCELLULAR LOCATION: Secreted.
CC   -! SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is clearly stated. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
Cc CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC CC
Dr DR EMBL: L20863; AAAA1809.1; -.
Dr DR EMBL: U09193; AAA79231.1; -.
Dr DR HSPS: P03451; ILIT.
Dr DR InterPro: IPRO01304; Lectin_C.
Dr DR InterPro: IPRO03990; Pancreatins_ac.
Dr Dr Pfam: PF00059; lectin_c_1.
Dr DR PRINTS: PR01504; PNCREARTNSAP.
Dr DR SMART: SM00034; CLCCT_1.
Dr DR PROSITE: PS00615; C-TYPE_LLECTIN_1; FALSE_NEG.
Dr DR PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
KW Signal; Lectin; Inflammatory response; Acute phase.
FT FT CHAIN          1             26            POTENTIAL.
FT FT MAIN          27            174          PANCREARTNIS-ASSOCIATED PROTEIN 3.
FT FT DOMAIN        38            172          C-TYPE LECTIN (LONG FORM).
FT FT DISULFID       40            51            BY SIMILARITY.
FT FT DISULFID       68            170          BY SIMILARITY.
FT FT DISULFID       145           162          BY SIMILARITY.
SQ     SEQUENCE      174 AA; 19143 MW; 5CED2E887C46E45C CRC64;
-----
Query Match                               54.1%; Score 518; DB 1; Length 174;
Best local Similarity 52.9%; Pred. No. 5; gpe-38;
Matches 92; Conservative 39; Mismatches 41; Indels 2; Gaps 2
```

DB	121	EMSNADVANNYNNWENP5-SVSGSHCGTLTAFASGFLRRENNCISELPPYCKFK	173
RESULT_9			
PAP2_RAT			
ID	PAP2_RAT	STANDARD:	PRT: 174 AA.
AC	P35231:		
DT	01-FEB-1994 (Rel. 28, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Pancreatitis-associated protein 2 precursor (lithostathine 3) (Islet of langerhans regenerating protein 3) (REG 3).		
OS	PAP2 OR REG3.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Pancreas;		
RX	MEDLINE=93378971; PubMed=8369291;		
RA	Frigerio J.-M., Dusetti N.J., Kelm V., Dagorn J.C., Iovanna J.L.,		
RT	"Identification of a second rat pancreatitis-associated protein,"		
RT	Messenger RNA cloning, gene structure, and expression during acute		
RL	pancreatitis.";		
RN	Biochemistry 32:9236-9241(1993).		
RP	[2]		
RC	SEQUENCE FROM N.A.		
RC	STRAIN=Mistar;		
RA	MEDLINE=94314238; PubMed=8039722;		
RA	Suzuki Y., Yonekura H., Watanabe T., Umno M., Morizumi S.,		
RT	Miyashita H., Okamoto H.;		
RT	"Structure and expression of a novel rat RegIII gene,"		
RL	Gene 144:315-316(1994).		
CC	- I- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF		
CC	BACTERIAL PROLIFERATION.		
CC	- I- SURCELLULAR LOCATION: Secreted.		
CC	- I- TISSUE SPECIFICITY: LOW EXPRESSION FOUND IN HEALTHY PANCREAS.		
CC	- I- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF		
CC	PANCREATIC INFLAMMATION.		
CC	- I- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.		
CC	- I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/		
CC	or send an email to license@sdb.ch).		
CC	-----		
DR	EMBL; L10230; AAAA1808.1; -		
DR	EMBL; L10229; AAA02980.1; -		
DR	EMBL; D26078; BAA05071.1; -		
DR	EMBL; D23676; BAA04904.1; -		
DR	PIR; A48689; A48689.		
DR	HSSP; P05451; 1LIT.		
DR	InterPro; IPR001304; Lectin_C.		
DR	InterPro; IPR003990; Pancreatitis_ac.		
DR	Pfam; PF000059; Lectin_c; 1.		
DR	PRINTS; PR01504; PNCREATTITSAF.		
DR	SMART; SM00034; CLECT; 1.		
DR	SMART; SM00615; C_TYPE_LECTIN_1; 1.		
DR	PROSITE; PS50041; C_TYPE_LECTIN_2; 1.		
KW	Signal; Lectin; Inflammatory protein phase.		
FT	SIGNAL	1	25
FT	CHAIN	26	174
FT	DOMAIN	37	172
FT	DISULEID	39	50
FT	DISULEID	67	170
FT	DISULEID	145	162
FT	CONFLICT	104	104
FT	SEQUENCE	174 AA; 19599 MW; 4530EB8449E5588 CRC64;	

Query	Match	Best Local Similarity	Score	DB	Length
Matches	74	Conservative	34	Mismatches	50
Indels	5	Gaps	1		
Db	11	WMLISLAMELWVEGESOKLPSSRITCPQGSVAAGSYCSYLILPOTSMNALSQOMH	70		
Db	8	FMLISSMLSLISQOGESESTELPNRISCPGTNAKNSYCYFNEDEPTWVDLDCQNM	67		
QY	71	ESGHLAEFLISTGHTITFVSSLVKNSLTAAYOYIMLGLDPSHQTLPNGSGWSSSNVLTREY	130		
Db	68	NSGNLSVLTQAEFGAFVSLIKESSTDSDSNWIGLHDPK-----KNRMHSSGSLYSK	122		
QY	131	NMERNPISIAADRGYCAVLISQSGPKMDFCENELPYICKK	173		
Db	123	SMDTGSPSSANAGYCASLTSCGFKKMDCEKRFVCKFK	165		
RESULT 11					
LITH RAT					
ID	LITH RAT	STANDARD:	PRT:	165 AA.	
AC	P10758;				
DT	01-JUL-1989 (Rel. 11, created)				
DT	01-JUL-1989 (Rel. 11, last sequence update)				
DT	15-JUN-2002 (Rel. 41, last annotation update)				
DE	Lithostreine precursor (Pancreatic stone protein) (PSP) (Pancreatic				
DE	thread protein) (PTP) (Islet of Langerhans regenerating protein) (REG				
DE	(Reg1 cells regeneration factor) (ICRF).				
GN	REG1 OR REG.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_Taxid=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91093273; PubMed=1985964;				
RA	Rouquier S., Verdier J.M., Iovanna J., Dagorn J.-C., Giorgi D.,				
RT	"Rat pancreatic stone protein messenger RNA. Abundant expression in				
RT	mature exocrine cells, regulation by food content, and sequence				
RT	identity with the endocrine reg transcript.";				
RT	J. Biol. Chem. 266:786-791(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8115343; PubMed=2963000;				
RA	Terao K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y.,				
RA	Tochino Y., Okamoto H.;				
RT	"A novel gene activated in regenerating islets.";				
RT	J. Biol. Chem. 263:2111-2114(1988).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=93326645; PubMed=7916640;				

```

RA Duseti N.J., Frigerio J.M., Daeron J.-C., Iovanna J.L.;
RT "rapid PCR cloning and sequence determination of the rat
RL 11tostathine gene.";
RN Blochim. Biophys. Acta 1174:99-102(1993).
RA [4]
RC SEQUENCE FROM N.A.
RA STRAIN-Wistar;
RA Miyashita H., Suzuki Y., Watanabe T., Uno M., Morizumi S.,
RT "Structure and characterization of rat Reg I gene.";
RL Saitagaku 65:1082-1082(1993).
RN [5]
RP SEQUENCE OF 22-69.
RC TISSUE=Pancreas;
RX MEDLINE=90031455; PubMed=2680252;
RA "Adich Z., de Caro A.M., Guidoni A.A., Woudstra M.E., Rovey M.;
RT "Characterization in rat pancreatic juice of a protein homologous to
RL the human pancreatic stone protein.";
RC Comp. Biochem. Physiol. 93B:793-797(1989).
CC -1- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM
CC CARBOXYATE PRECIPITATION.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN REGENERATING ISLETS, BUT
CC NOT IN NORMAL PANCREATIC ISLETS, INSULINOMAS OR REGENERATING
CC LIVER.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-slb.ch/announce/
CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL, L07512; AAA41533.1; -
DR EMBL, M62930; AAA41974.1; -
DR EMBL, M18962; AAA41978.1; -
DR EMBL, D26164; BA005149.1; -
DR PIR, A28351; A28351.
DR PIR, PL0147; PL0147.
DR PIR, A39081; A39081.
DR PIR, S34618; S34618.
DR HSSP, P05451; LITP.
DR InterPro: IPR001304; Lectin.C.
DR InterPro: IPR003990; Pancreatlis_ac.
DR Pfam: PF00059; Lectin_c.1.
DR PRINTS: PR01504; PNCREATLISAP.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
KM Glycoprotein; Signal; Lectin.
FT SIGNAL 1 21
FT CHAIN 22 165 LITHOSTATHINE.
FT DOMAIN 33 163 C-TYPE LECTIN (LONG FORM).
FT DISULFID 35 46 BY SIMILARITY.
FT DISULFID 63 161 BY SIMILARITY.
FT DISULFID 136 153 BY SIMILARITY.
FT CARBOHYD 129 129 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 165 AA; 18672 MW; 9B61EB236B82CF8A CR664;

Query Match 41.3%; Score 395.5; DB 1; Length 165;
Best local Similarity 44.2%; Pred. No. 2e-27;
Matches 72; Conservative 35; Mismatches 51; Indels 5; Gaps 1

OY 11 WALISCLMFLSWGEGESSOKKIPSRITCGSGVAAGSYCYSLILLPQTMNAELSCOMH 70
DB 7 FILISCLMVLSPSGOGAEEDLPARITCEGSNAISSTCYTYMEDHLSMAEDLFCQNA 66
OY 71 FSGHIAFLITSGETITFVSSLVKNSLITAYQYIWIWGLDHPDGHGLPNSGKWSNNVLTFF 130
DB 67 NSGLIVLVSQABENFTLASLIKESGTTAAVWVWIGLHDPK-----NNRRWMSGSGSLFLYK 121
OY 131 NWERNPISIAADRGYCAVLISOKSGFGQKRDRNCERHELPTICKFK 173

```

[illegible]

```

RESULT 13
LIT2_MOUSE STANDARD; PRT; 173 AA.
ID LIT2_MOUSE
AC 008731;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lithostathine 2 precursor (Pancreatic stone protein 2) (PSP)
DE (Pancreatic thread protein 2) (PTP) (Islet of Langerhans regenerating
DE protein 2) (REG 2).
GN REG2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=93340209; PubMed=8340418;
RA Uno M., Yonekura H., Nakagawara K.-I., Watanabe T., Miyashita H.,
RA Morizumi S., Okamoto H., Itoh T., Teraoka H.;
RT "Structure, chromosomal localization, and expression of mouse reg
RT genes, reg I and reg II. A novel type of reg gene, reg II, exists in
RT the mouse genome."
RL J. Biol. Chem. 268:15974-15982(1993).
CC -1- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIDIUM
CC CARBONATE PRECIPITATION.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN REGENERATING ISLETS AND
CC NORMAL EXOCRINE PANCREAS, BUT NOT IN NORMAL PANCREATIC ISLETS.
CC EXPRESSED STRONGLY IN PANCREAS, WEAKLY IN LIVER, BUT NOT AT ALL
CC IN GALLBLADDER.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: D14011; BAA03112.1; -.
DR HSSP: P05451; ILIT.
DR MGD: MGI:97896; Reg2.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR003990; Pancreatis_ac.
DR Pfam: PF00059; Lectin_C; 1.
DR PRINTS: PR01504; PNCREARIT5AP.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
KW Signal; Lectin.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 173 LITHOSTATHINE 2.
FT DOMAIN 41 171 C-TYPE LECTIN (LONG FORM).
FT DISULFID 43 54 BY SIMILARITY.
FT DISULFID 71 169 BY SIMILARITY.
FT DISULFID 144 161 BY SIMILARITY.
SQ SEQUENCE 173 AA; 19407 MW; 7D34CDAB232F25C CRC64;

Query Match 40.3%; Score 386; DB 1; Length 173;
Best Local Similarity 43.8%; Pred. No. 1.4e-26;
Matches 74; Conservative 28; Mismatches 55; Indels 12; Gaps 3;

```

```

QY 12 MISCAMFISWEG--EE-----SOKLPSRINTPOGSAVGYSCYSLILIPOTWMAE 64
DB 9 ILELCMFSTYSOGVAEDPFLAEDPESAKINCPESGANNIGSYCYLLIEDRLTWGEAD 68
QY 65 LSCOMFSGHALLSTGRTITVSSIVKNSLTAAYOYITGLHDPESHGTLFPGSGKWSSS 124
DB 69 LFCQNNAGHLVSLISQAESNFVASLIVKESGTTASNVMTGLHDPK-----SNRRWMSGS 123

```

```

QY 125 NVLTFYNNERNPSIADRGYCAVLSQKSGFQKMDPNCENELPYICKFK 173
DB 124 SLFLKSWATGAPSPANRGYCVSLTSNTAYKKWMDENCEAGYVCKFR 172

RESULT 14
LIT1_HUMAN STANDARD; PRT; 166 AA.
ID LIT1_HUMAN
AC P05451; P11379;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lithostathine 1 alpha precursor (Pancreatic stone protein) (PSP)
DE (Pancreatic thread protein) (PTP) (Islet of Langerhans regenerating
DE protein) (REG) (Regenerating protein 1 alpha) (Islet cells
DE regeneration factor) (ICRF).
GN REG1A OR REG OR PSPS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN 11;
RP SEQUENCE FROM N.A.
RX MEDLINE=88115343; PubMed=2963000;
RA Teraono K., Yamamoto H., Takasawa S., Shiga K., Yonemura Y.,
RA Tochino Y., Okamoto H.;
RT "A novel gene activated in regenerating islets."
RL J. Biol. Chem. 263:2111-2114(1988).
RN 12;
RP SEQUENCE FROM N.A.
RX MEDLINE=90237042; PubMed=2332435;
RA Watanabe T., Yonekura H., Teraono K., Yamamoto H., Okamoto H.;
RT "Complete nucleotide sequence of human reg gene and its expression in
RT normal and tumoral tissues. The reg protein, pancreatic stone
RT protein, and pancreatic thread protein are one and the same product
RT of the gene."
RL J. Biol. Chem. 265:7432-7439(1990).
RN 13;
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=89292148; PubMed=2525567;
RA Giorgi D., Bernard J.-P., Rouquier S., Iovanna J., Sarles H.,
RA Dagorn J.-C.;
RT "Secretory pancreatic stone protein messenger RNA. Nucleotide
RT sequence and expression in chronic calcifying pancreatitis."
RL J. Clin. Invest. 84:100-106(1989).
RN 14;
RP SEQUENCE FROM N.A.
RA Boonyaisawat W., Tandhanand-Banchulin N., Vannasaeng S.,
RA Yenchitsomansat P.;
RT Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN 15;
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN 16;
RP SEQUENCE OF 34-166.
RX MEDLINE=88029417; PubMed=3665916;
RA de Caro A.M., Bonicel J.J., Roult P., de Caro J.D., Sarles H.,
RA Roverly M.;
RT "Complete amino acid sequence of an immunoreactive form of human
RT pancreatic stone protein isolated from pancreatic juice."
RL Eur. J. Biochem. 168:201-207(1987).
RN 17;
RP SEQUENCE OF 34-98.
RX MEDLINE=87099550; PubMed=3541906;
RA Montali G., Bonicel J.J., Mulligner L., Roverly M., Sarles H.,
RA de Caro A.M.;
RT "Partial amino acid sequence of human pancreatic stone protein, a
RT novel pancreatic secretory protein."
RL Biochem. J. 238:227-232(1986).
RN 18;

```


LIT1_MOUSE STANDARD; PRT; 165 AA.
ID LIT1_MOUSE
AC P43137;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lithostathine 1 precursor (Pancreatic stone protein 1) (PSP)
DE (Pancreatic thread protein 1) (PTP) (Islet of Langerhans regenerating
DE protein 1) (REG 1).
GN REG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC -STRAIN=C57BL/6J;
RX MEDLINE=93340209; PubMed=8340418;
RA Uno M., Yonekura H., Nakagawa K.-I., Watanabe T., Miyashita H.,
RA Morizumi S., Okamoto H., Itoh T., Terakita H.,
RT "Structure, chromosomal localization, and expression of mouse reg
RT genes, reg I and reg II. A novel type of reg gene, reg II, exists in
RT the mouse genome."
RL J. Biol. Chem. 268:15974-15982(1993).
CC -1- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM
CC CARBONATE PRECIPITATION.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN REGENERATING ISLETS AND
CC NORMAL EXOCRINE PANCREAS, BUT NOT IN NORMAL PANCREATIC ISLETS.
CC EXPRESSED STRONGLY IN PANCREAS, MODERATELY IN GALLBLADDER, AND
CC WEAKLY IN LIVER.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: D14010; BAA03111.1; -.
CC DR HSSP; P05451; LIT.
CC DR MGI: 97895; Reg1.
CC DR InterPro: IPR001304; Lectin_C.
CC DR InterPro: IPR003990; Pancreatis_ac.
CC DR Pfam: PF00059; Lectin_cf_1.
CC DR PRINTS; PR01504; PNCREATITSAP.
CC DR SMART; SM00034; CLECT; 1.
CC DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
CC DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
CC KW Glycoprotein; Signal; Lectin.
CC FT SIGNAL 1 21 BY SIMILARITY.
CC FT CHAIN 1 165 LITHOSTATHINE 1.
CC FT DOMAIN 33 163 C-TYPE LECTIN (LONG FORM).
CC FT DISULFID 35 46 BY SIMILARITY.
CC FT DISULFID 63 161 BY SIMILARITY.
CC FT DISULFID 136 153 BY SIMILARITY.
CC FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SQ SEQUENCE 165 AA; 18518 MW; 2950174AF5D666BA CRC64;
Query Match 39.7%; Score 380.5; DB 1; Length 165;
Best Local Similarity 42.3%; Pred. No. 3.9e-26;
Matches 69; Conservative 35; Mismatches 54; Indels 5; Gaps 1;
OY 11 WMLSLMFLSWVEEESGKRLPSRITCPGSGVAYGSGYSLILLIPOTWSNAFLSCOMH 70
DB 7 FILISCLIVLSPSGQEARFEDLPKARISCPBSNAYSSCYTFEDRLIMADADLFCOMM 66
OY 71 FSGHLAFLISTGEITFVSSLVNLSLTAYQYIWLIGLHDPSSHGLPNSGGMKSSNVLTFF 130
DB 67 NSGYLAVSYLSQAEGNFVSLIKESGTDANWYTGILHDPK-----RNRMRHWSGSLFLYK 121
OY 131 NWRNRPSTADRGCAVLSSQKSGFQKWRDFNCENLPIYCKFK 173

Db 122 SWATGSPNNSNRGCVSLTSNTGKRWKMDNCDAQYSFYCKFK 164

Search completed: April 16, 2003, 10:46:44
Job time : 14 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:43:30 ; Search time 32 Seconds
(without alignments)
1120.381 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 1 MDPMTLCRMSTMLSCMLF.....QKWRDNCENELPYCKFKV 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mnc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	750	78.3	138	11	09QYF7 mesocricetu
2	676	70.6	175	11	09JMH1 09qus9 mus musculu
3	676	70.6	175	11	09QUS9 09cyf4 mus musculu
4	437	45.6	146	11	09QYF8 09qy18 mus musculu
5	360	37.6	98	11	09QYF8 09qy18 mus musculu
6	277	28.9	86	11	09COB4 09qy18 mus musculu
7	246.5	25.7	157	11	09DBS8 09d85 mus musculu
8	244.5	25.5	157	11	09DBS5 09d85 mus musculu
9	196	20.5	152	13	09DG39 09d39 agkistrodon
10	194	20.3	158	13	09QW17 09q17 bungarus fa
11	191	19.9	158	13	08UYC6 08uc6 agkistrodon
12	190	19.8	152	13	09IAM1 09iam1 agkistrodon
13	190	19.8	158	4	09BYZ8 09byz8 homo sapien
14	184	19.2	158	13	09QW18 09qw18 bungarus fa
15	184	19.2	158	13	09QW16 09qw16 bungarus mu
16	183	19.1	146	13	09DEF8 09def8 agkistrodon

17	182	19.0	152	13	09DEF9 09def9 agkistrodon
18	180	18.8	146	13	09DC31 09dc31 agkistrodon
19	179	18.7	146	13	09IAM0 09iam0 agkistrodon
20	178	18.6	146	13	09I840 09i840 agkistrodon
21	176	18.4	146	13	09BUJ0 09bujo trimeresuru
22	172	18.0	134	5	09XYX3 09xyx3 hydra magni
23	171.5	17.9	136	13	09I841 09i841 agkistrodon
24	171	17.8	124	13	09BSM5 09bsm5 agkistrodon
25	169	17.6	134	5	09UB05 09ub05 hydra atten
26	169	17.6	134	5	025199 025199 hydra atten
27	168.5	17.6	135	13	09PSM4 09psm4 laecheis mu
28	168	17.5	134	5	09XYX2 09xyx2 hydra atten
29	166.5	17.4	145	13	09YGN4 09ygn4 agkistrodon
30	166	17.3	134	5	09XYX4 09xyx4 hydra Olig
31	166	17.3	154	13	09YGN5 09ygn5 agkistrodon
32	165.5	17.3	157	13	09YGN5 09ygn5 agkistrodon
33	164.5	17.2	2109	13	P79787 09ygn5 agkistrodon
34	164.5	16.9	148	13	093427 093427 crotales du
35	162	16.9	1722	4	075913 075913 homo sapien
36	161.5	16.9	155	13	09DER2 09dea2 agkistrodon
37	161	16.8	1722	4	060449 060449 homo sapien
38	160	16.7	166	13	09QWJ8 09qwj8 anguilla ja
39	158.5	16.5	315	4	09UPK6 09upk6 homo sapien
40	158.5	16.5	1321	4	014594 014594 homo sapien
41	158.5	16.5	1723	11	060767 060767 mus musculu
42	158.5	16.5	1723	11	091X18 091x18 mus musculu
43	157	16.4	1479	11	064449 064449 mus musculu
44	156.5	16.3	1487	11	062028 062028 mus musculu
45	156	16.3	1326	4	Q13019 013019 homo sapien

ALIGNMENTS

RESULT 1
ID 09QYF7 PRELIMINARY: PRT; 138 AA.
AC 09QYF7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Islet neogenesis associated protein (Fragment).
GN INGP.
OS Mesocricetus auratus (golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231736; PubMed=10767532;
RA Abe M., Nara K., Akiyama T., Shervani N.J., Kobayashi S.,
RA Tomioka-Kumagai T., Ito S., Takasawa S., Okamoto H.,
RT "Identification of a novel Reg family gene, Reg III delta, and mapping
RT of all three types of Reg family gene in a 75 kilobase mouse genomic
RT region.";
RL Gene 246:111-122(2000).
DR EMBL: AB035211; BAAB8566.1; -
DR HSSP: P05451; IOPD.
DR InterPro: IPR000282; Cytok_receptor_2.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LECTIN_1; 1.
DR PROSITE: PS00041; C_TYPE_LECTIN_2; 1.
FT NON_TER
SQ SEQUENCE 138 AA: 15585 MW: 453888AADIIB524 CRC64;
Query Match 78.3%; Score 750; DB 11; Length 138;
Best Local Similarity 98.6%; Pred. NO. 5.4e-67;
Matches 136; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 37 ITCPGSAVAGSYCYSLIIIPQTSNAELSCOMHPSGHILATLSTGELTFVSLVKSLT 96

```

Db 1 ITPOGSAVAGSYCYSLILIPQWNAELSCQMFHSCHLFLSTGTITFVSSILVKNLSLT
QY 97 AYOTWGLDPSHGTPNGSGWKNSSNLTFFYNERNPSIADRGCAVLSQKSGFQK 156
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 61 AYOTWGLDPSHGTPNGSGWKNSSNLTFFYNERNPSIADRGCAVLSQKSGFQK 120
QY 157 WRDNCENELPYICKFKV 174
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 121 WRDNCENELPYICKFKV 138

RESULT 2
Q9JMH1 PRELIMINARY; PRT; 175 AA.
ID 09JMH1
AC 09JMH1
DT 01-OCT-2000 (Tremblrel, 15, Created)
DT 01-OCT-2000 (Tremblrel, 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel, 19, Last annotation update)
DE INGP related protein.
GN INGP OR INGPAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BDF-1; TISSUE=DUODENUM;
RX MEDLINE=20033449; PubMed=10564727;
RA Sasahara K., Yamoka T., Moritani M., Yoshimoto K., Kuroda Y.,
  Itakura M.;
RT "Molecular cloning and tissue-specific expression of a new member of
  the regenerating protein family, Islet neogenesis-associated protein-
  related protein.";
RL Biochim. Biophys. Acta 1500:142-146(2000).
DR EMBL: AB028625; BAA92141.1; -.
DR HSSP: P05451; IQDD.
DR MGD: MGI:1353426; Ingapp.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C.1.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 175 AA; 20021 MW; 0A92FA6112BC6B53 CRC64;

Query Match 70.6%; Score 676; DB 11; Length 175;
Best Local Similarity 72.2%; Pred. No. 1.6e-59;
Matches 122; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 5 TLRMSMMLSCIMPLSWVEGESQKRLPSSRTCPQGSVAVGSCYCYSLILIPQWNAE 64
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 6 TLRMSMMLSCIMPLSWVGEQSKRLSPRISCPQEAQVGYCYCYLLILEPQWNAE 65
QY 65 LSCQMFHSCHLFLSTGTITFVSSLVKNSLTAYQYTWGLDPSHGTPNGSGWKNSS 124
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 66 IHQCKHFSGLAFLLTYGELTFVSSLVKNSLTFFPYTWGLDPSHGTPNGSGWKNSS 125
QY 125 NVLTFYNERNPSIADRGCAVLSQKSGFQKWRDNCENELPYICKFK 173
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 126 DPLTFNWEIPPSMAHGYCALSQASGYQKRDYCDITFFYVCKF 174

RESULT 3
Q9QUS9 PRELIMINARY; PRT; 175 AA.
ID 09QUS9
AC 09QUS9;
DT 01-MAY-2000 (Tremblrel, 13, Created)
DT 01-MAY-2000 (Tremblrel, 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel, 20, Last annotation update)
DE REG III delta precursor (Islet neogenesis associated protein-related
  protein).
GN INGPAP OR REG3D.
OS Mus musculus (Mouse).

```

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Abe M., Nata K., Tomioka-Kumagai T., Takasawa S., Ito S., Okamoto H.;
RT "Identification of a novel Reg family gene, Reg III delta, and mapping
  of all three types of Reg family genes in 75-kilobase mouse genomic
  region.";
RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
  Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
  Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
  Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
  Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
  Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
  Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
  Schirml L.M., Straubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
  Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
  Blake J., Botfield D., Boyle N., Carninci P., de Bonaldo M.F.,
  Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
  Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
  Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
  Nordone P., Ring B., Schoenbach M., Rodriguez I., Sakamoto N.,
  Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
  Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Winkler L.,
  Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AB035204; BAA88564.1; -.
DR EMBL: AB035205; BAA88565.1; -.
DR EMBL: AK019033; BAB31518.1; -.
DR HSSP: P05451; IQDD.
DR MGD: MGI:1353426; Ingapp.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR003990; Pancreatins_ac.
DR Pfam: PF00059; Lectin_C.1.
DR PRINTS: PR01504; PNCREATITSAF.
DR SMART: SM00034; CLECT.1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 175 AA; 20037 MW; 0A88D67512BC6B53 CRC64;

Query Match 70.6%; Score 676; DB 11; Length 175;
Best Local Similarity 72.2%; Pred. No. 1.6e-59;
Matches 122; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

QY 5 TLRMSMMLSCIMPLSWVEGESQKRLPSSRTCPQGSVAVGSCYCYSLILIPQWNAE 64
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 6 TLRMSMMLSCIMPLSWVGEQSKRLSPRISCPQEAQVGYCYCYLLILEPQWNAE 65
QY 65 LSCQMFHSCHLFLSTGTITFVSSLVKNSLTAYQYTWGLDPSHGTPNGSGWKNSS 124
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 66 IHQCKHFSGLAFLLTYGELTFVSSLVKNSLTFFPYTWGLDPSHGTPNGSGWKNSS 125
QY 125 NVLTFYNERNPSIADRGCAVLSQKSGFQKWRDNCENELPYICKFK 173
  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
Db 126 DPLTFNWEIPPSMAHGYCALSQASGYQKRDYCDITFFYVCKF 174

RESULT 4
Q9CVF4 PRELIMINARY; PRT; 146 AA.
ID 09CVF4
AC 09CVF4;
DT 01-JUN-2001 (Tremblrel, 17, Created)
DT 01-JUN-2001 (Tremblrel, 17, Last sequence update)

```

02	10000000
RN	[1]

```
DR InterPro: IPR001304: Lectin C.
DK MBL, MGI:105408, Reg3a:
DK MBL, MGI:105408, Reg3a:
```

00 Mammalia, Eulimella, Scutogaster, Mollusc, Mus:
01 NCBI TAXID=10090;
02

DR HSSP; P05451; 1QDD.

RN	[1]	
RN		

DR Pfam: PF00059; lectin_c.1.
 DR PROSITE: PS00615; C_Type_Lectin_1; 1.
 DR PROSITE: PS00611; C_Type_Lectin_2; 1.
 FT NON-TER 1 1

SO SEQUENCE 86 AA; 9575 MW; 98088079FC357EB CRC64;

Query Match 28.9%; Score 277; DB 11; Length 86;
 Best Local Similarity 52.9%; Pred. No. 3.5e-17;
 Matches 45; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 89 SLVKNLSITAYOYIWGLDPSHGTLPLNGSGKMWSSNVLTFTYWRNPISADRGCAVL 148
 ID 09D858; PRELIMINARY; PRT; 157 AA.
 AC 09D858;
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE 2010002115Rik protein.
 GN 2010002115Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK008438; BAB25669.1; -
 DR HSSP: P05451; 10DD.
 DR MGD: MGI:1914959; 2010002115Rik.
 DR InterPro: IPR001304; lectin_c.1.
 DR Pfam: PF00059; lectin_c.1.
 DR SMART: SM00034; CLECT_1.
 DR PROSITE: PS00611; C_Type_Lectin_2; 1.
 DR PROSITE: PS00615; C_Type_Lectin_1; 1.
 SO SEQUENCE 157 AA; 18474 MW; FD96F36CFB989368 CRC64;

Query Match 25.7%; Score 246.5; DB 11; Length 157;
 Best Local Similarity 32.5%; Pred. No. 7.5e-17;
 Matches 55; Conservative 30; Mismatches 67; Indels 17; Gaps 6;

QY 9 MSMLLSCLMFLSMWEGESQKRLPSRRITCPQGSVAAGSYCYSLILPQWTSNAELSCQ 68
 ID 09D858; PRELIMINARY; PRT; 157 AA.
 AC 09D858;
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, last annotation update)
 DE 2010002115Rik protein.
 GN 2010002115Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]

QY 69 MHRSSG-HLAFILSTGEITFVSSLVKNLSITAYOY---IWIGLHDPSTGLPLNGSGKMWSS 124
 ID 09D858; PRELIMINARY; PRT; 157 AA.
 AC 09D858;
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE 2010002115Rik protein (RIKEN cDNA 2010002115 gene).
 GN 2010002115Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
 RA Hayashizaki Y.,
 RT Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK008438; BAB25429.1; -
 DR HSSP: P05451; 10DD.
 DR MGD: MGI:1914959; 2010002115Rik.
 DR InterPro: IPR001304; lectin_c.1.
 DR Pfam: PF00059; lectin_c.1.
 DR SMART: SM00034; CLECT_1.
 DR PROSITE: PS00611; C_Type_Lectin_2; 1.
 DR PROSITE: PS00615; C_Type_Lectin_1; 1.
 SO SEQUENCE 157 AA; 18398 MW; F3981722BDB83968 CRC64;

Query Match 25.5%; Score 244.5; DB 11; Length 157;
 Best Local Similarity 33.5%; Pred. No. 1.2e-16;
 Matches 54; Conservative 27; Mismatches 63; Indels 17; Gaps 6;

QY 17 IMFLSMWEGESQKRLPSRRITCPQGSVAAGSYCYSLILPQWTSNAELSCOMHFSQ-HL 75
 ID 09D858; PRELIMINARY; PRT; 157 AA.
 AC 09D858;
 DT 01-JUN-2001 (TrEMBLrel. 17, last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, last annotation update)
 DE 2010002115Rik protein (RIKEN cDNA 2010002115 gene).
 GN 2010002115Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]

QY 133 ERNPSIADRGCAVLSQSGFQKWDENCENELPYCKE 173
 DB 118 --NPRTESEARHCAMFPMKDKFLTNKNCANROHFLCKYK 156

RESULT 9

Q9DG39 PRELIMINARY; PRT: 152 AA.

AC Q9DG39; 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE Halysin A-chain precursor.

GN HXNA.

OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
 OC Viperidae; Crotalinae; Gloydius.

OX NCBI_TaxID=8714;

RN [1]

RP SEQUENCE FROM N.A.

RA Koo B.H., Sohn Y.D., Kim D.S., Jang Y.S., Chung K.H.;

RT "A novel coagulation factor Xa inhibitor from Korean snake

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF190827; AAG17178.1; -.

DR HSSP; P23806; 11XX.

DR InterPro; IPR001304; Lectin_C.

DR Pfam; PF00059; Lectin_C; 1.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.

DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

KW Signal.

FT SIGNAL. 1 23

FT CHAIN 24 23 POTENTIAL.

FT SIGNAL 1 23 HALYXIN A-CHAIN.

SO SEQUENCE 152 AA; 17455 MW; BDD74D1DC280C28D CRC64;

Query Match 20.5%; Score 196; DB 13; Length 152;
 Best Local Similarity 30.3%; Pred. No. 7.7e-12;

Matches 50; Conservative 32; Mismatches 61; Indels 22; Gaps 7;

QY 9 MSWMLSCIMFLMVEEESQKRLPSSRTICPGSGVAVSYCYSLILIPQWNAELSCQ 68
 DB 7 LSEFL--VFLS-----LSGTGADCSGMSSTGHCYINFLFKTMAEERPCR 54

QY 69 MPEFG-HLAFLLSTGETTFVSSLVKNSLTAYQ-YIMIGLHDSHGTLPNGSGMKWSSNV 126
 DB 55 KOVGAHLVIESSEEDAFVQALVSEMKRYGIYIWIGLR--VRGKKKCCS-QMSDSS 111

QY 127 LTFYMERNPISIAADRGCAVLSQSGFQKWDENCENELPYCK 171
 DB 112 VSYQNM-----IEASTKICIGLOKTEFRKWNITYGGENPVCE 151

RESULT 10

Q90W17 PRELIMINARY; PRT: 158 AA.

AC Q90W17; 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)

DT 01-MAR-2002 (Tremblrel. 20, last annotation update)

DE C-type lectin-like protein 2.

OS Bungarus fasciatus (Banded krait).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;

OC Elapidae; Bungarinae; Bungarus.

OX NCBI_TaxID=8613;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=VENOM GLAND;

RA Zha H.-G., Zhang Y.;

"CDNA cloning and characterization of C-type lectin-like proteins from

RT Elapidae snakes.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF354271; AAK43585.1; -.

DR InterPro; IPR001304; Lectin_C.

DR Pfam; PF00059; Lectin_C; 1.

DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.

DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

KW Lectin.

SO SEQUENCE 158 AA; 18254 MW; 5F0218970DA17453 CRC64;

Query Match 19.9%; Score 191; DB 13; Length 158;
 Best Local Similarity 29.6%; Pred. No. 1.3e-11;

Matches 48; Conservative 26; Mismatches 68; Indels 18; Gaps 6;

QY 16 CL--WFLSWVEEESQKRLPSSRTICPGSGVAVSYCYSLILIPQWNAELSCQMHESG 73
 DB 10 CLTAMFLS--LSGAE-----YTCPLDWLPKNGLCYKFSNPKSMJDAEMFCRKFPG 60

QY 74 -HLAFLSTGETTFVSSLVKNSLTAYQYIMIGLHDSHGTLPNGSGMKWSSNVLTFFNM 132
 DB 61 CHLASIHRDADSDLAERYSDYLDKDDGNVWIGLNDPQ-----KKRTWVMSDRSSNYFEM 115

QY 133 ERNPSIADRGCAVLSQSGFQKWDENCENELPYCKE 173
 DB 116 NQEPFNSKNEYCYHMAFPTGLKMDAPCETLHPYCKCK 157

RESULT 11

Q80VC6 PRELIMINARY; PRT: 158 AA.

AC Q80VC6; 20, Created)

DT 01-MAR-2002 (Tremblrel. 20, last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, last annotation update)

DE Antichrombin 1 A chain.

OS Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;

OC Viperidae; Crotalinae; Deinagkistrodon.

OX NCBI_TaxID=36307;

RN [1]

RP SEQUENCE FROM N.A.

RA Yu H., Xiang K., Liu J.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF463522; AAL6391.1; -.

DR InterPro; IPR001304; Lectin_C.

DR Pfam; PF00059; Lectin_C; 1.

DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.

DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.

SO SEQUENCE 158 AA; 17950 MW; A73A9C895997BFD7 CRC64;

Query Match 19.9%; Score 191; DB 13; Length 158;
 Best Local Similarity 30.7%; Pred. No. 2.5e-11;

Matches 43; Conservative 24; Mismatches 55; Indels 18; Gaps 5;

QY 39 CPQGSVAVSYCYSLILIPQWNAELSC-OMHPSGHLAFLSTGETTFVSSLVKNSLTA 97
 DB 27 CPFGMSAYQCYCYIKPKKNMDDAERCFEQADGHLVSIESGGEEDFAQLVSGSIS 86

QY 98 YQ-YIMIGLHDSHGTLPNGSGMKWSSNVLTFFN-----WERNPSIADRGCAVLSQGS 152
 DB 87 VEDHWVTGILRVONK--EKQSTWSDSSVSVENLDELTYMRK-----CGALERET 134

QY 153 GFQKWRDFNCENELPYCKE 172
 DB 135 GFHKWINTLCIOLNPFVCKE 154

RESULT 12

Q91AM1 PRELIMINARY; PRT: 152 AA.

AC Q91AM1;

DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Agkistrodon A chain.
 OS Agkistrodon acutus (Hundred-pace snake) (Delnagkistrodon acutus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Delnagkistrodon.
 NC NCBITaxid=36307;
 RN- [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM;
 RA Yu H.-X., Xiang K.-J., Liu J.;
 RT "cDNA sequencing and analysis of eleven C-type lectin-like protein
 subunits from Agkistrodon acutus."
 RT Chin. J. Biochem. Biophys. 0:0-0(2002).
 DR EMBL: AF176420; AAF26286.2; -; 76A0F636BFD07AB CRC64;
 SQ SEQUENCE 152 AA; 17109 MW; 76A0F636BFD07AB CRC64;

Query Match 19.8%; Score 190; DB 13; Length 152;
 Best Local Similarity 27.4%; Pred. No. 3e-11;
 Matches 43; Conservative 32; Mismatches 62; Indels 20; Gaps 5;

QY 17 MLTSLAFVWEEGSEQKLPSSRITCPQGSVAAGSYCYSLILIPQWMAELSCOMHFS-GHL 75
 DB 13 VVFLS-----LSGTADCCSSGWSYEGHCKYVKOSKRTWDASFCTKQVNGHL 62
 QY 76 AFLTSTGETTFVSVLVKNSL-TAYQYIWLGHDPHSGTLPNGSGKMWSSNVLTFFYMER 134
 DB 63 VSIESSEGEAFVQGLIAOKIKSAKIHVMIGLMAQNK--EKQCSIEWSDGSSISYEMW-- 117
 QY 135 NPSTIADRGCAVLISQKSGFQKWRDPCNENELPYICK 171
 DB 118 ---IEESKCKLGVHETGFKMENFYCEQDPEYCE 151

RESULT 13
 Q9BYZ8 PRELIMINARY; PRT; 158 AA.

AC Q9BYZ8;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Regenerating gene type IV (Regenerating gene type IV precursor)
 DE (Gastrointestinal secretory protein GISP).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBITaxid=9606;
 RN- [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=21210973; PubMed=11311942;
 RA Hartup J.C., Zhang H., Bonaldo M.F., Soares M.B., Dieckgraefe B.K.;
 RT "Isolation and characterization of a cDNA encoding a novel member of
 the human regenerating protein family: Reg IV(1)."
 RL Biochim. Biophys. Acta 1518:287-293(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON CANCER;
 RA Violette S., Fesfor E., Dussaux E., Citadelle D., Chamaz J.;
 RT "The new intestinal Reg IV gene is involved in drug-resistance of
 colon tumor cells."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Strausberg R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Lin W.-C.;
 RT "Identification of gastrointestinal secretory protein (GISP), a new

RT member of lithostathine gene family."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY007243; AA602562.1; -;
 DR EMBL: AF345934; AA59869.1; -;
 DR EMBL: BC017089; AAH17089.1; -;
 DR EMBL: AF254415; AAK48435.1; -;
 DR HSSP: P05451; 10DD.
 DR InterPro: IPR001304; Lectin C.
 DR InterPro: IPR003990; Pancreatis_ac.
 DR Pfam: PF00059; Lectin_C_1; Lectin C.
 DR PRINTS: PRO1504; PROKATITAP.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
 DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
 RT Signal.
 FT SIGNAL.
 SQ SEQUENCE 158 AA; 18230 MW; 7308849CBBDE93E CRC64;

Query Match 19.8%; Score 190; DB 4; Length 158;
 Best Local Similarity 30.1%; Pred. No. 3.2e-11;
 Matches 50; Conservative 28; Mismatches 66; Indels 22; Gaps 8;

QY 12 MLTSLAFVWEEGSEQKLPSSRITCPQGSVAAGSYCYSLILIPQWMAELSCOMHFS 71
 DB 10 LLSCLA-KTGYLDIIL-----RPGCAQWGFYHKNCGYFRKLRLNNSDALECGSYG 62
 QY 72 SG-HLAFSTGETTFVSVLVKNSL-TAYQYIWLGHDPHSGTLPNGSGKMWSSNVLTFFYMER 127
 DB 63 NHAHLASTLSKE---ASTAETYSIGQNSQPIWELHDPQ-----KROQWQMDGAMT 113
 QY 128 PFYMERNPSTIADRGCAVLISQKSGFQKWRDPCNENELPYICK 173
 DB 114 LYRSMN-GKSMGKNC-HCAEMSSNNNFLTSSNCCNKRQHLCKYR 157

RESULT 14
 Q90W18 PRELIMINARY; PRT; 158 AA.

AC Q90W18;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE C-type lectin-like protein 1.
 OS Bungarus fasciatus (Banded krait).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Bungarinae; Bungarus.
 NC NCBITaxid=8613;
 RN- [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RA Zha H.-G., Zhang Y.;
 RT "cDNA cloning and characterization of C-type lectin-like proteins from
 Elapidae snakes."
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF354270; AAK43584.1; -;
 DR InterPro: IPR001304; Lectin_C.
 DR Pfam: PF00059; Lectin_C_1.
 DR PROSITE: PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.
 DR PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
 KW Lectin.
 SQ SEQUENCE 158 AA; 18638 MW; ECF8593FMA182B8 CRC64;

Query Match 19.2%; Score 184; DB 13; Length 158;
 Best Local Similarity 28.4%; Pred. No. 1.2e-10;
 Matches 46; Conservative 27; Mismatches 71; Indels 18; Gaps 6;

QY 16 CL--WFLSWVEGSEQKLPSSRITCPQGSVAAGSYCYSLILIPQWMAELSCOMHFSG 73
 DB 10 CLIAFLS-LSAEC-----YTCTPDWLPKNGCTKYPSKRTYFDAMCTKRFKRG 60
 QY 74 HLAFSTGETTFVSVLVKNSL-TAYQYIWLGHDPHSGTLPNGSGKMWSSNVLTFFYMER 132
 DB 63 NHAHLASTLSKE---ASTAETYSIGQNSQPIWELHDPQ-----KROQWQMDGAMT 113

Db 61 CHLASLHNSNADAVEFSEYISDYITGSGHWIGIRDTKKYI-----WETDRSRTPFLPW 115
QY 133 -ERNPSTIADRGYCAVLISOKSGFQKWRDPNCENELPYICKER 173
Db 116 RKKOPDHFNNEFCVEIVNFTGYLQWNDNCALRPFLCQCK 157

RESULT 15

Q90W16 PRELIMINARY; PRT; 158 AA.
AC Q90W16;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE C-type lectin-like protein 1.
OS Bungarus multiclincus (Many-banded krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OX NCBI_TaxID=8616;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Zha H.-G., Zhang Y.;
RT "cDNA cloning and characterization of C-type lectin-like proteins from
RT Elapidae snakes".
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF354272; AAK43586.1; -.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; lectin_c; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; UNKNOWN_1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW lectin.
SQ SEQUENCE 158 AA; 18706 MW; 66B71A29D104805 CRC64;

Query Match 19.2%; Score 184; DB 13; Length 158;
Best Local Similarity 29.0%; Pred. No. 1.2e-10;
Matches 47; Conservative 25; Mismatches 72; Indels 18; Gaps 6;

QY 16 CL-MFLSWVEGESOKLPSSRITCPQGSVAYGSYCSLLIPQWTSNAELSCOMHFSG 73
Db 10 CLAMFLS-LRGAEC-----YTCPIDWLPKNGLCYKVFSGHKHTWPDAEKCYCKRFG 60
QY 74 -HLAFLSTGEITFVSSLVNNSITAYQIYIWIGLHDPHSGTLPNGSGWKSSNVLTFTNW 132
Db 61 CHLASLHNSNADAVEFSEYISDYITGSGHWIGIRDTKKYI-----WETDRSRTPFLPW 115
QY 133 ERN-PSIADRGYCAVLISOKSGFQKWRDPNCENELPYICKER 173
Db 116 RKNQPDHFNNEFCVEIVNFTGYLQWNDNCALRPFLCQCK 157

Search completed: April 16, 2003, 10:47:23
Job time : 34 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:45:50 ; Search time 28 Seconds
(Without alignments)

182.842 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 1 MPTLCRMSSMLSLCLMFL.....QKWRDPCENELPYCKEKV 174

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents-AI.*
1: /cgn2.6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2.6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2.6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2.6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2.6/ptodata/1/1aa/PCtus-COMB.pep.*
6: /cgn2.6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	958	100.0	174	2	US-08-401-530A-2
2	958	100.0	174	2	US-08-709-662-2
3	958	100.0	175	1	US-08-909-725-6
4	598	62.4	175	2	US-08-401-530A-3
5	598	62.4	175	2	US-08-709-662-3
6	572	59.7	175	2	US-08-464-637-2
7	572	59.7	175	2	US-08-401-530A-4
8	572	59.7	175	2	US-08-709-662-4
9	572	59.7	175	2	US-08-822-261-3
10	566	59.1	174	1	US-07-778-156-7
11	566	59.1	174	2	US-08-822-261-4
12	566	59.1	174	2	US-08-422-166-7
13	557	58.1	175	2	US-08-822-261-1
14	557	58.1	184	1	US-07-778-156-2
15	557	58.1	184	1	US-08-422-166-2
16	518	54.1	174	2	US-08-401-530A-5
17	518	54.1	174	2	US-08-709-662-5
18	464	50.5	158	1	US-07-778-156-3
19	464	50.5	158	2	US-08-422-166-3
20	466	48.6	174	2	US-08-401-530A-6
21	466	48.6	174	2	US-08-709-662-6
22	402.5	42.0	166	2	US-08-729-103-4
23	395.5	41.3	165	2	US-08-401-530A-7
24	395.5	41.3	165	2	US-08-729-103-3
25	395.5	41.3	165	2	US-08-709-662-7
26	257.5	20.1	117	6	5514562-15
27	193	20.1	134	1	US-07-893-929A-2

28	193	20.1	134	5	PCT-US92-10344-2	Sequence 2, Appl1
29	190	19.8	158	2	US-08-729-103-1	Sequence 1, Appl1
30	190	19.8	158	2	US-08-468-413-2	Sequence 2, Appl1
31	190	19.8	158	3	US-09-162-508-2	Sequence 2, Appl1
32	190	19.8	158	3	PCT-US95-07169-2	Sequence 2, Appl1
33	185	19.3	131	1	US-07-893-929A-1	Sequence 1, Appl1
34	185	19.3	131	5	PCT-US92-10344-1	Sequence 1, Appl1
35	172	18.0	130	1	US-07-893-929A-7	Sequence 7, Appl1
36	172	18.0	133	1	PCT-US92-10344-7	Sequence 7, Appl1
37	172	18.0	133	1	US-07-893-929A-9	Sequence 9, Appl1
38	172	18.0	133	5	PCT-US92-10344-9	Sequence 9, Appl1
39	164	17.1	125	1	US-07-893-929A-3	Sequence 3, Appl1
40	164	17.1	125	5	PCT-US92-10344-3	Sequence 3, Appl1
41	162	16.9	132	1	US-07-893-929A-5	Sequence 5, Appl1
42	162	16.9	132	5	PCT-US92-10344-5	Sequence 5, Appl1
43	161	16.8	172	4	US-09-194-612A-1	Sequence 1, Appl1
44	160	16.7	123	1	US-07-893-929A-4	Sequence 4, Appl1
45	160	16.7	123	5	PCT-US92-10344-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1
US-08-401-530A-2
Sequence 2, Application US/08401530A
Patent No. 5834590.

GENERAL INFORMATION:

APPLICANT: Vink, Aaron I.
APPLICANT: Piltenger, Gary L.
APPLICANT: Rataeloff, Ronit
APPLICANT: Rosenber, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
NUMBER OF INVENTIONS: 1
TITLE OF INVENTION: ISLET NEOGENESIS

CORRESPONDENCE ADDRESS:

ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington

STATE: D.C.

COUNTRY: US

ZIP: 20001-4597

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/401,530A

FILING DATE: 22-FEB-1995

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A. 32,141

REGISTRATION NUMBER: 00570.48743

REFERENCE/DOCKET NUMBER: 00570.48743

TELEPHONE: 202-508-9299

TELEFAX: 202-508-9299

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 174 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-401-530A-2

Query Match 100.0%; Score 958; DB 2; Length 174;

Best local Similarity 100.0%; Pred. No. 2.7e-98;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MPTLCRMSSMLSLCLMFLSWGEGESQKRLPSRTCGSGVAAGSYSLILPQW 60

Db 1 MLPTLCRSMWMLSCIMFLSMVGEESQKLPSSRTICPOGSAVAGSYCSLILIPQW 60
QY 61 SNAELSCQMHFSGHLAFLLSTGEITFVSSLVKNLSLTAYQYIWIIGLHDPSSHGTLPNNGSGWK 120
Db 61 SNAELSCQMHFSGHLAFLLSTGEITFVSSLVKNLSLTAYQYIWIIGLHDPSSHGTLPNNGSGWK 120
QY 121 WSSSNVLTFFYNMERNPSTIADRGCAVLSQKSGFQKMRDFNCENELPYICKFKV 174
Db 121 WSSSNVLTFFYNMERNPSTIADRGCAVLSQKSGFQKMRDFNCENELPYICKFKV 174

RESULT 2

US-08-709-662-2
; Sequence 2, Application US/08709662
; Patent No. 5840531
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Pittenger, Gary L.
; APPLICANT: Rafaeloff, Ronit
; APPLICANT: Rosenberg, Lawrence
; APPLICANT: Duguid, William P.
; TITLE OF INVENTION: ISLET PROTEIN INVOLVED IN PANCREATIC
; TITLE OF INVENTION: ISLET NEOGENESIS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: US
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/709,662
; APPLICATION NUMBER: 09-SEP-1996
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,141
; REFERENCE/DOCKET NUMBER: 00570,59178
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-709-662-2

Query Match 100.0%; Score 958; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No. 2,7e-98;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPTLCRSMWMLSCIMFLSMVGEESQKLPSSRTICPOGSAVAGSYCSLILIPQW 60
Db 1 MLPTLCRSMWMLSCIMFLSMVGEESQKLPSSRTICPOGSAVAGSYCSLILIPQW 60
QY 61 SNAELSCQMHFSGHLAFLLSTGEITFVSSLVKNLSLTAYQYIWIIGLHDPSSHGTLPNNGSGWK 120
Db 61 SNAELSCQMHFSGHLAFLLSTGEITFVSSLVKNLSLTAYQYIWIIGLHDPSSHGTLPNNGSGWK 120
QY 121 WSSSNVLTFFYNMERNPSTIADRGCAVLSQKSGFQKMRDFNCENELPYICKFKV 174
Db 121 WSSSNVLTFFYNMERNPSTIADRGCAVLSQKSGFQKMRDFNCENELPYICKFKV 174

RESULT 3

RESULT 3

US-08-909-725-6
; Sequence 6, Application US/08909725
; Patent No. 5804421
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Pittenger, Gary
; APPLICANT: Rafaeloff-Phall, Ronit
; APPLICANT: Barlow, Scott
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
; TITLE OF INVENTION: INCAP IN BACTERIAL AND EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 1001 G Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/909,725
; FILING DATE: 12-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/741,096
; FILING DATE: 30-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A.
; REGISTRATION NUMBER: 32,145
; REFERENCE/DOCKET NUMBER: 0570,05173
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: 97430 BMB UT
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-909-725-6

Query Match 100.0%; Score 958; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 2,8e-98;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPTLCRSMWMLSCIMFLSMVGEESQKLPSSRTICPOGSAVAGSYCSLILIPQW 60
Db 2 MLPTLCRSMWMLSCIMFLSMVGEESQKLPSSRTICPOGSAVAGSYCSLILIPQW 61
QY 61 SNAELSCQMHFSGHLAFLLSTGEITFVSSLVKNLSLTAYQYIWIIGLHDPSSHGTLPNNGSGWK 120
Db 61 SNAELSCQMHFSGHLAFLLSTGEITFVSSLVKNLSLTAYQYIWIIGLHDPSSHGTLPNNGSGWK 120
QY 121 WSSSNVLTFFYNMERNPSTIADRGCAVLSQKSGFQKMRDFNCENELPYICKFKV 174
Db 121 WSSSNVLTFFYNMERNPSTIADRGCAVLSQKSGFQKMRDFNCENELPYICKFKV 175

RESULT 4
US-08-401-530A-3
; Sequence 3, Application US/08401530A
; Patent No. 5834590
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Pittenger, Gary L.
; APPLICANT: Rafaeloff, Ronit
; APPLICANT: Rosenberg, Lawrence

US-08-401-530A-3

APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
City: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-401-530A-3

Query Match 62.4%; Score 598; DB 2; Length 175;
Best Local Similarity 61.6%; Pred. No. 1.8e-58;
Matches 101; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 9 MSMLSLCLMFLSWGESEOKLPSSRTCPGSAVAGSYCYSLILPOTWNAELSCQ 68
DB 10 MSMLSLCLMFLSQVGEDSPKIPSAISCPKSGQAVGSCYALPOTWDAELACQ 69
QY 69 MFSGLAFLSTGEITFVSSLVKNSLTAYQYIWIGLHDPHSHGTLPNGSGMKWSSNVLT 128
DB 70 KRPEGHVSLVAVASFLASMKNTGNSYQYIWIGLHDPHTLGEPRNGGEMWNSNDIMN 129
QY 129 FYWNERPSTIADRGYCAVLISOKSGFOKWRDNCENELPYICKE 172
DB 130 YVWNERPSTALDRGFCGSLSSGFLMRDITCEVAKLPYCKF 173

RESULT 5
US-08-709-662-3
Sequence 3, Application US/08709662
Patent No. 5840531
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron I.
APPLICANT: Piltenger, Gary L.
APPLICANT: Ratajecki, Ronald
APPLICANT: Rosendberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
City: Washington
STATE: D.C.

COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rattus rattus
US-08-709-662-3

Query Match 62.4%; Score 598; DB 2; Length 175;
Best Local Similarity 61.6%; Pred. No. 1.8e-58;
Matches 101; Conservative 30; Mismatches 33; Indels 0; Gaps 0;

QY 9 MSMLSLCLMFLSWGESEOKLPSSRTCPGSAVAGSYCYSLILPOTWNAELSCQ 68
DB 10 MSMLSLCLMFLSQVGEDSPKIPSAISCPKSGQAVGSCYALPOTWDAELACQ 69
QY 69 MFSGLAFLSTGEITFVSSLVKNSLTAYQYIWIGLHDPHSHGTLPNGSGMKWSSNVLT 128
DB 70 KRPEGHVSLVAVASFLASMKNTGNSYQYIWIGLHDPHTLGEPRNGGEMWNSNDIMN 129
QY 129 FYWNERPSTIADRGYCAVLISOKSGFOKWRDNCENELPYICKE 172
DB 130 YVWNERPSTALDRGFCGSLSSGFLMRDITCEVAKLPYCKF 173

RESULT 6
US-08-464-637-2
Sequence 2, Application US/08464637
Patent No. 5834214
GENERAL INFORMATION:
APPLICANT: Iovanna, Juan-Luicio
APPLICANT: Dagorn, Jean-Charles
APPLICANT: Keim, Volker
APPLICANT: Saries, Jacques
TITLE OF INVENTION: Detection of Pancreatitis-Associated
TITLE OF INVENTION: Protein for Diagnosis of Cystic Fibrosis or Pancreatic
TITLE OF INVENTION: Disease (as amended).
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
City: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,637

FILING DATE: 30-AUG-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Murphy Jr., Gerald M.
 REGISTRATION NUMBER: 28,977
 REFERENCE/DOCKET NUMBER: 2121-107P
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-205-8000
 TELEFAX: 703-205-8050
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 175 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-464-637-2

Query Match 59.7%; Score 572; DB 2; Length 175;
 Best Local Similarity 57.6%; Pred. No. 1,4e-55;
 Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

QY 3 PMTICRMSMMLSCIMLMSVGEESQKLPSSRITCPQGSVAVGYCYSLILIPQWMSN 62
 || : ||||| || : ||||| || : ||||| || : ||||| || : ||||| || : |||||
 DB 4 PMALPSVSMMLSCIMLMSVQGEPEQRELPARIRCPKSGKAYGSHCYALFLSPKSWTD 63
 QY 63 AELSCOMHSGHIAFLSTGETFPVSSLYKNSLTAQYIWIIGLHDPHSGTLPNGSGMKMS 122
 || : ||||| || : ||||| || : ||||| || : ||||| || : ||||| || : |||||
 DB 64 ADLACOKRPSGNLYSLGAEGSFVSLVKSIGNSYTWIGLHDPGTGTEPNGBEWMWS 123
 QY 123 SSNVLTFFYMERNPISIAADRGICAVLSQSGFQKWRDPCENELPYICKF 172
 || : ||||| || : ||||| || : ||||| || : ||||| || : ||||| || : |||||
 DB 124 SSDVMNYFAMERNPSTISSPGHCASLSRSTAFLEMKDYNQCNVRLPYCKF 173

RESULT 7
 US-08-401-530A-4
 Sequence 4, Application US/08401530A
 Patent No. 5834550
 GENERAL INFORMATION:
 APPLICANT: Vink, Aaron I.
 APPLICANT: Pittenger, Gary L.
 APPLICANT: Rafaeloff, Ronit
 APPLICANT: Rosenberg, Lawrence
 APPLICANT: Duguid, William P.
 TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Allegretti
 STREET: 1001 G Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: US
 ZIP: 20001-4597
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/401,530A
 FILING DATE: 22-FEB-1995
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Kagan, Sarah A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 00570,48743
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9299
 TELEFAX: 202-508-9299
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 175 amino acids

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-401-530A-4

Query Match 59.7%; Score 572; DB 2; Length 175;
 Best Local Similarity 57.6%; Pred. No. 1,4e-55;
 Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

QY 3 PMTICRMSMMLSCIMLMSVGEESQKLPSSRITCPQGSVAVGYCYSLILIPQWMSN 62
 || : ||||| || : ||||| || : ||||| || : ||||| || : ||||| || : |||||
 DB 4 PMALPSVSMMLSCIMLMSVQGEPEQRELPARIRCPKSGKAYGSHCYALFLSPKSWTD 63
 QY 63 AELSCOMHSGHIAFLSTGETFPVSSLYKNSLTAQYIWIIGLHDPHSGTLPNGSGMKMS 122
 || : ||||| || : ||||| || : ||||| || : ||||| || : ||||| || : |||||
 DB 64 ADLACOKRPSGNLYSLGAEGSFVSLVKSIGNSYTWIGLHDPGTGTEPNGBEWMWS 123
 QY 123 SSNVLTFFYMERNPISIAADRGICAVLSQSGFQKWRDPCENELPYICKF 172
 || : ||||| || : ||||| || : ||||| || : ||||| || : ||||| || : |||||
 DB 124 SSDVMNYFAMERNPSTISSPGHCASLSRSTAFLEMKDYNQCNVRLPYCKF 173

RESULT 8
 US-08-709-662-4
 Sequence 4, Application US/08709662
 Patent No. 5840531
 GENERAL INFORMATION:
 APPLICANT: Vink, Aaron I.
 APPLICANT: Pittenger, Gary L.
 APPLICANT: Rafaeloff, Ronit
 APPLICANT: Rosenberg, Lawrence
 APPLICANT: Duguid, William P.
 TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
 NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Banner & Witcoff, Ltd.
 STREET: 1001 G Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: US
 ZIP: 20001-4597
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,662
 FILING DATE: 09-SEP-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kagan, Sarah A.
 REGISTRATION NUMBER: 32,141
 REFERENCE/DOCKET NUMBER: 00570,59178
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9299
 TELEFAX: 202-508-9299
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 175 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 US-08-709-662-4

Query Match 59.7%; Score 572; DB 2; Length 175;
 Best Local Similarity 57.6%; Pred. No. 1,4e-55;
 Matches 98; Conservative 34; Mismatches 38; Indels 0; Gaps 0;


```

; Patent No. 5935813
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,261
; FILING DATE: Filed Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0251 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 189601
;
US-08-822-261-4
;
Query Match 59.1%; Score 566; DB 2; Length 174;
Best Local Similarity 57.4%; Pred. No. 6.3e-55;
Matches 97; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

QY 3 PNTLCRMSMMLSCIMLTSMWEGESOKKLPSSRTTCPOGSVAAGSYCSILLIPOTMSN 62
DB 4 PMLALPSVSMMLSCIMLTSMWEGESOKKLPSSRTTCPOGSVAAGSYCSILLIPOTMSN 63
QY 63 AELSCOMHFSGLHFLSTGEITFYVSSLVKNLSLTAAYQYIWIIGLHDPHSHGTLPNSSGMKMS 122
DB 64 ADLAQCKRRSPGSLVSLGAGSGSVSSLYKSGNSYIWIIGLHDPHSHGTLPNSSGMKMS 123
QY 123 SSNVLTFTYFNWERNPSIAADRGYCAVLISOKSGFQKWRDPNCENELPYICK 171
DB 124 SSDVMNIFAMERNPSTISSPGHCASLSRSTAFILMKDYNCNVRILPYICK 172

RESULT 12
US-08-422-166-7
; Sequence 7, Application US/08422166
; Patent No. 5959086
; GENERAL INFORMATION:
; APPLICANT: Iovanna, Juan-Lucio
; APPLICANT: Keim, Volker
; APPLICANT: Dagorn, Jean-Charles
; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
; TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
; TITLE OF INVENTION: PANCREATITIS
; NUMBER OF SEQUENCES: 12
```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Obion, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,166
; FILING DATE: 14-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/778,156
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Obion, No. 5959086man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 354-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 174 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; ORIGIN: Homo sapiens
; ORGANISM: Homo sapiens
; TISSUE TYPE: pancreas
;
US-08-422-166-7
;
Query Match 59.1%; Score 566; DB 2; Length 174;
Best Local Similarity 57.4%; Pred. No. 6.3e-55;
Matches 97; Conservative 34; Mismatches 38; Indels 0; Gaps 0;

QY 3 PNTLCRMSMMLSCIMLTSMWEGESOKKLPSSRTTCPOGSVAAGSYCSILLIPOTMSN 62
DB 4 PMLALPSVSMMLSCIMLTSMWEGESOKKLPSSRTTCPOGSVAAGSYCSILLIPOTMSN 63
QY 63 AELSCOMHFSGLHFLSTGEITFYVSSLVKNLSLTAAYQYIWIIGLHDPHSHGTLPNSSGMKMS 122
DB 64 ADLAQCKRRSPGSLVSLGAGSGSVSSLYKSGNSYIWIIGLHDPHSHGTLPNSSGMKMS 123
QY 123 SSNVLTFTYFNWERNPSIAADRGYCAVLISOKSGFQKWRDPNCENELPYICK 171
DB 124 SSDVMNIFAMERNPSTISSPGHCASLSRSTAFILMKDYNCNVRILPYICK 172

RESULT 13
US-08-822-261-1
; Sequence 1, Application US/08822261
; Patent No. 5935813
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Goli, Surya K.
; TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
```


COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE: Filed Herewith
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0251 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: ISLNOT01
CLONE: 2072483
US-08-822-261-1

Query Match 58.1%; Score 557; DB 2; Length 175;
Best Local Similarity 55.6%; Pred. No. 6,2e-54;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

QY 3 PMTLCRSMWMLSCIMELFWGEESQKLPSSRTICPOGSVAAGSYCYSLILIPQWMSN 62
DB 4 PMALPSYMWLSCILLCVOGEETQKLPSPRISCRGSKAIGSPCYALFLSPKSMMD 63
QY 63 AELSCMHPSGHFLAFLSTGETTFVSSLVKNLSLAYOYIWIHLDPHSHGLPNSSGKMS 122
DB 64 ADLACOKRPSGKLYSLVSAEGSEFVSSLVRSISNSYIWIHLDPHPTGSEPDGDGEMWS 123
QY 123 SSNVLFFYMERNPSTIADRGCAVLISQKSGFQKWRDNCENELPYICKFK 173
DB 124 STDVMTFMEKRPSTIILNPHGCSLSRSTGLKNDKDKALPYVCKFK 174

RESULT 14
US-07-778-156-2
Sequence 2, Application US/07778156
Patent No. 5436169
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBOLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/778,156
FILING DATE: 19911219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Obolon, No. 5436169man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248855 OPART UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-778-156-2

Query Match 58.1%; Score 557; DB 1; Length 184;
Best Local Similarity 60.1%; Pred. No. 6,7e-54;
Matches 95; Conservative 29; Mismatches 34; Indels 0; Gaps 0;

QY 9 MSWMLSCIMELFWGEESQKLPSSRTICPOGSVAAGSYCYSLILIPQWMSNLSQ 68
DB 10 MSWMLSCIMLSQYQGDSPKIPSAKISCPKSGQASGYCYALPQIPTWFDALAQ 69
QY 69 MHPSGHFLAFLSTGETTFVSSLVKNLSLAYOYIWIHLDPHSHGLPNSSGKMSNVLT 128
DB 70 KRREGHLVSLNVAASLASLAKNKGNSYQYIWIHLDPHSHGLPNSSGKMSNVLT 129
QY 129 FYMERNPSTIADRGCAVLISQKSGFQKWRDNCENELPYICKFK 166
DB 130 YNWERNPSTIADRGCAVLISQKSGFQKWRDNCENELPYICKFK 167

RESULT 15
US-08-422-166-2
Sequence 2, Application US/08422166
Patent No. 5959086
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBOLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Obolon, No. 5959086man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:

Wed Apr 16 12:14:48 2003

us-08-401-530-2.rai

Page 8

```

: TELEPHONE: (703)521-4500
: TELEFAX: (703)486-2347
: TELEX: 248855 OAT UR
: INFORMATION FOR SEQ ID NO: 2
: SEQUENCE CHARACTERISTICS:
: LENGTH: 164 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
:
: US-08-422-166-2

```

Query Match 58.1%; Score 557; DB 2; Length 184;
Best Local Similarity 60.1%; Pred. No. 6.7e-54;
Matches 95; Conservative 29; Mismatches 34; Indels 0; Gaps 0;

QY	9	MSMMLLSCMLPFLSWEJGESORRKPSSRRICPPGQSAVSYSCYSHILLPQWNAEILASCO	68
Db	10	MSMMLLSCMLPFLSWEJGESORRKPSSRRICPPGQSAVSYSCYSHILLPQWNAEILASCO	69
QY	69	MHRSGHAFLLTGTGETVSSLYNNSLTAAVOYIMIGLHPHSQTLPPNSGKMWSSNVL	128
Db	70	KRREGLHLYLVNALASLTASLAWKNTGNSOYIYIMIGLHPDLTGLGERNGSGMWSNIDLM	129
QY	129	FYWEERNPSTADRCYCAVLSQKSGFOKMRDFNCENFL	166
Db	130	YVWEERNPSTADRCYCAVLSQKSGFOKMRDTCCEV	167

Search completed: April 16, 2003, 10:48:21
Job time : 29 secs

GenCore version 5.1.4-P5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:46:30 ; Search time 18 seconds
(Without alignment cell updates/sec
730.934 Million cell updates/sec)

Title: US-08-401-530-2

Perfect score: 958
Sequence: 1 MIPMTICRSMWMLSCIMFL.....QKWRDENCENELPYICKRV 174

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 288829 seqs, 75613885 residues

Total number of hits satisfying chosen parameters: 288829

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep: *
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep: *
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep: *
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep: *
5: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep: *
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep: *
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep: *
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep: *
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep: *
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep: *
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep: *
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep: *
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep: *
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	572	59.7	183	10	US-09-925-301-1013 Sequence 1013, App
2	557	58.1	175	9	US-09-978-285A-452 Sequence 452, App
3	557	58.1	175	9	US-09-978-697-452 Sequence 452, App
4	557	58.1	175	9	US-09-978-192A-452 Sequence 452, App
5	557	58.1	175	9	US-09-999-832A-452 Sequence 452, App
6	557	58.1	175	9	US-09-978-189-452 Sequence 452, App
7	557	58.1	175	9	US-10-174-590-424 Sequence 424, App
8	557	58.1	175	9	US-10-176-758-424 Sequence 424, App
9	557	58.1	175	9	US-10-175-737-424 Sequence 424, App
10	557	58.1	175	9	US-10-173-706-424 Sequence 424, App
11	557	58.1	175	9	US-10-173-728-424 Sequence 424, App
12	557	58.1	175	9	US-10-173-752-424 Sequence 424, App
13	557	58.1	175	9	US-10-176-482-424 Sequence 424, App
14	557	58.1	175	9	US-10-176-757-424 Sequence 424, App
15	557	58.1	175	9	US-10-176-913-424 Sequence 424, App
16	557	58.1	175	9	US-10-180-552-424 Sequence 424, App
17	557	58.1	175	9	US-10-180-557-424 Sequence 424, App
18	557	58.1	175	9	US-10-173-700-424 Sequence 424, App
19	557	58.1	175	9	US-10-174-572-424 Sequence 424, App

20	557	58.1	175	9	US-10-174-579-424 Sequence 424, App
21	557	58.1	175	9	US-10-174-582-424 Sequence 424, App
22	557	58.1	175	9	US-10-174-588-424 Sequence 424, App
23	557	58.1	175	9	US-10-175-739-424 Sequence 424, App
24	557	58.1	175	9	US-10-175-740-424 Sequence 424, App
25	557	58.1	175	9	US-10-175-743-424 Sequence 424, App
26	557	58.1	175	9	US-10-176-488-424 Sequence 424, App
27	557	58.1	175	9	US-10-176-492-424 Sequence 424, App
28	557	58.1	175	9	US-10-176-747-424 Sequence 424, App
29	557	58.1	175	9	US-10-176-750-424 Sequence 424, App
30	557	58.1	175	9	US-10-176-985-424 Sequence 424, App
31	557	58.1	175	9	US-10-176-987-424 Sequence 424, App
32	557	58.1	175	9	US-10-176-991-424 Sequence 424, App
33	557	58.1	175	9	US-10-176-992-424 Sequence 424, App
34	557	58.1	175	9	US-10-176-993-424 Sequence 424, App
35	557	58.1	175	9	US-10-184-658-424 Sequence 424, App
36	557	58.1	175	9	US-10-173-695-424 Sequence 424, App
37	557	58.1	175	9	US-10-173-697-424 Sequence 424, App
38	557	58.1	175	9	US-10-173-705-424 Sequence 424, App
39	557	58.1	175	9	US-10-174-576-424 Sequence 424, App
40	557	58.1	175	9	US-10-174-585-424 Sequence 424, App
41	557	58.1	175	9	US-10-174-586-424 Sequence 424, App
42	557	58.1	175	9	US-10-174-747-424 Sequence 424, App
43	557	58.1	175	9	US-10-176-481-424 Sequence 424, App
44	557	58.1	175	9	US-10-176-485-424 Sequence 424, App
45	557	58.1	175	9	US-10-176-487-424 Sequence 424, App

ALIGNMENTS

RESULT 1
US-09-925-301-1013
; Sequence 1013, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1013
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1013

Query Match	59.7%	Score 572;	DB 10;	Length 183;
Best Local Similarity	57.6%	Pred. No. 9.2e-50;		
Matches 98;	Conservative 34;	Mismatches 38;	Indels 0;	Gaps 0;
QY	3	PMTICRSMWMLSCIMFLSWGESESOQKLPSSRITCPQGSVAGSYCYSLIIPQWSEN 62		
DB	12	PALPSVSMWMLSCIMFLSWGESESOQKLPSSRITCPQGSVAGSYCYSLIIPQWSEN 71		
QY	63	AELSCOMFSGHIAFLSTGEITFVSVLVNSLTAAYITWIGLHDSHETLPNGSMKWS 122		
DB	72	ADLACQKRPSSGNLVSLSGATGFSVSVLSVNSLTAAYITWIGLHDSHETLPNGSMKWS 131		
QY	123	SSNVLTFFYMERNPISADRGCAVLSQSGKGFQKWRDENCENELPYICKRV 172		
DB	132	SSDVNMYFAWERNPSTISSPGHCASLRSRTAFLEMKDYNCNVALPYCKVF 181		
RESULT 2				
US-09-978-295A-452				
; Sequence 452, Application US/09978295A				

Patent No. US70020156006A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerder, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Iyar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC11
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663

PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29

;; PRIOR APPLICATION NUMBER: 60/083545
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083554
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083558
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083559
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083500
;; PRIOR FILING DATE: 1998-04-29
;; PRIOR APPLICATION NUMBER: 60/083742
;; PRIOR FILING DATE: 1998-04-30
;; PRIOR APPLICATION NUMBER: 60/084366
;; PRIOR FILING DATE: 1998-05-05
;; PRIOR APPLICATION NUMBER: 60/084414
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084441
;; PRIOR FILING DATE: 1998-05-06
;; PRIOR APPLICATION NUMBER: 60/084637
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084639
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084640
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 58.1%; Score 557; DB 9; Length 175;
Best Local Similarity 55.6%; Pred. No. 2.8e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;
QY 3 PWTICMSNMLSLCLMFLTSWVEGESOKKLPSSRTCPQGSVAVAGSYCSYLIPQWMSN 62
DB 4 PMAIPSVNMLSLCLLQVOGEFQKLPSPRISCKPKSKAVGSPCYALFLSPKXMD 63
QY 63 AELSCOMHSHGLAFLTSGELTYVSSLYKNSLTAYQITWGLDHPISGHTLPNSSGKMS 122
DB 64 ADLACORRPSGKLVSLSABESFVSLVRSISNSTIYIGLHDPTQGSSEDDGEMWS 123
QY 123 SSNVLFYWNRPSTIADRGYCAVLSOKSGFQKWWDENCENELPYICKFK 173
DB 124 STDVNNYFAWEKNPSTILNPGHGSLSRGTGLFKKDYNCDAKLPYCKFK 174

RESULT 3
US-09-978-697-452

;; Sequence 452, Application US/09978697
;; Patent No. US20020169284A1
;; GENERAL INFORMATION:
;; APPLICANT: Askenazi, Avi
;; APPLICANT: Baker Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan
;; APPLICANT: Ferrara, Napoleon
;; APPLICANT: Flivaroff, Ellen
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gao, Wei-Qiang
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Geritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gunney, Austin J.
;; APPLICANT: Hillan, Kenneth J.
;; APPLICANT: Kiljavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PIC27
;; CURRENT APPLICATION NUMBER: US/09/978,697
;; PRIOR FILING DATE: 2001-10-16
;; PRIOR APPLICATION NUMBER: 09/918585
;; PRIOR FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/064249
;; PRIOR FILING DATE: 1997-11-03
;; PRIOR APPLICATION NUMBER: 60/065311
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/066364
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: 60/077450
;; PRIOR FILING DATE: 1998-03-10
;; PRIOR APPLICATION NUMBER: 60/077632
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077641
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077649
;; PRIOR FILING DATE: 1998-03-11
;; PRIOR APPLICATION NUMBER: 60/077791
;; PRIOR FILING DATE: 1998-03-12
;; PRIOR APPLICATION NUMBER: 60/078004
;; PRIOR FILING DATE: 1998-03-13
;; PRIOR APPLICATION NUMBER: 60/078886
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078936
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/078939
;; PRIOR FILING DATE: 1998-03-20
;; PRIOR APPLICATION NUMBER: 60/079294
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: 60/079656
;; PRIOR FILING DATE: 1998-03-26
;; PRIOR APPLICATION NUMBER: 60/079664
;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079689
;; PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499

PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/085339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085579
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

Query Match 58.1%; Score 557; DB 9; Length 175;
Best Local Similarity 55.6%; Pred. No. 2.8e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

QY 3 PPTICMSWMLSCIMFSLSWYBESOKKLPSSRITRQGSVAAGSCYULILPOTWSN 62
DB 4 PMLPSVSWMLSCILICVOVGEEFQKLPSPRISCPKSGAKAYGSPCALPFSKSWMD 63
QY 63 AELSCOMHPSGHIAFLSTGETFEVSSLYKNSLTAYOYIWTGLHDPHGTLFNGSGKWS 122
DB 64 ADLACQKRPSSGKLYSVLGAEGSFVSLVRSISNSYSYIWTGLHDPYQGSSEPDGDEWS 123
QY 123 SSNVLTFYWMENRPSIADRGYCAVLISQSGFQKWRDPENCENLPYICKRK 173
DB 124 SDVVMYFAWEKNPSTILNPGHGSLSRSTGFLMKDYKDCAKLPYICKRK 174
RESULT 4

US-09-978-192A-452
; Sequence 452, Application US/09978192A
; Patent No. US2002017753A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Flivaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978, 192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689

; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079663
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079920
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/079923
; PRIOR FILING DATE: 1998-03-30
; PRIOR APPLICATION NUMBER: 60/080105
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080165
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080328
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080334
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081071
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081229
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081952
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082700
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082796
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: 60/083336
; PRIOR FILING DATE: 1998-04-27
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/083392
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083496
; PRIOR FILING DATE: 1998-04-29

[illegible]

```

RESULT 5
US-09-999-832A-452
Sequence 452, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Ford, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsens, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27

```


[illegible]

RESULT 6
US-09-978-189-452
Sequence 452, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Flivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/07450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079656
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: 60/079664

PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079786
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/079923
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29

```

/ PRIOR APPLICATION NUMBER: 60/083496
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083499
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083545
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083554
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083558
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083559
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083500
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083742
/ PRIOR FILING DATE: 1998-04-30
/ PRIOR APPLICATION NUMBER: 60/084366
/ PRIOR FILING DATE: 1998-05-05
/ PRIOR APPLICATION NUMBER: 60/084414
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084441
/ PRIOR FILING DATE: 1998-05-06
/ PRIOR APPLICATION NUMBER: 60/084637
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084639
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084640
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084598
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084627
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084643
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/085339
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085338
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085323
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085582
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085700
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085580
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
/ PRIOR APPLICATION NUMBER: 60/085697

Query Match      58.1%; Score 557; DB 9; Length 175;
Best Local Similarity 55.6%; Pred. No. 2.8e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

QY 3 PHTLCMSMMLSCIMFISWVEGESOKKLPSSRTCPQSGVAAGYCSILIPQTMN 62
DB 4 PALPSVSMMLSCILLICOVGEETOKELPSRISCPKSGKAYGSPCYALFLSPKSMMD 63
QY 63 AELSCOMHPSGHLAFLSTGETTFVSSLVKNLSLAYOYIWIIGLDPHSHGTLPNNGSKWMS 122
DB 64 ADIACQKRRSGGLVSLGABSGFVSSLYRSISNSYIWIIGLDPHPTGSGPDDGHEMS 123
QY 123 SSNVLTFFYMERNPSTIAADRGYCAVLISQSGFQKWRDNCENELPYICKER 173
DB 124 STDVNMVFAMERNPSTILNPGHGSLSRSTGFLWKWDYNCDAKLPYICKER 174
```

```

RESULT 7
US-10-174-590-424
/ Sequence 424, Application US/10174590
/ Publication No. US2003008352A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Guiney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Zhang, Zemin I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C42
/ CURRENT APPLICATION NUMBER: US/10/174,590
/ PRIOR APPLICATION removed - See file Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 424
/ LENGTH: 175
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-174-590-424

Query Match      58.1%; Score 557; DB 9; Length 175;
Best Local Similarity 55.6%; Pred. No. 2.8e-48;
Matches 95; Conservative 37; Mismatches 39; Indels 0; Gaps 0;

QY 3 PHTLCMSMMLSCIMFISWVEGESOKKLPSSRTCPQSGVAAGYCSILIPQTMN 62
DB 4 PALPSVSMMLSCILLICOVGEETOKELPSRISCPKSGKAYGSPCYALFLSPKSMMD 63
QY 63 AELSCOMHPSGHLAFLSTGETTFVSSLVKNLSLAYOYIWIIGLDPHSHGTLPNNGSKWMS 122
DB 64 ADIACQKRRSGGLVSLGABSGFVSSLYRSISNSYIWIIGLDPHPTGSGPDDGHEMS 123
QY 123 SSNVLTFFYMERNPSTIAADRGYCAVLISQSGFQKWRDNCENELPYICKER 173
DB 124 STDVNMVFAMERNPSTILNPGHGSLSRSTGFLWKWDYNCDAKLPYICKER 174

RESULT 8
US-10-176-758-424
/ Sequence 424, Application US/10176758
/ Publication No. US2003008353A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Guiney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Zhang, Zemin I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE REFERENCE: P3430R1C104
/ CURRENT APPLICATION NUMBER: US/10/176,758
/ PRIOR APPLICATION removed - See file Wrapper or Palm
/ NUMBER OF SEQ ID NOS: 612
/ SEQ ID NO 424
/ LENGTH: 175
```


GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:46:51 ; Search time 36 seconds

(without alignments)
644.045 Million cell updates/sec

Title: US-08-401-530-2

Perfect score: 174

Sequence: 1 MIPMTLCRMSWMLSCIMFL.....QKWRDPCENELPYICKERY 174

Scoring table: OLIGO
Gapop 60.0 , Capext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 10

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A.Geneseq.101002.*

```

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
7: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
11: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*
12: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	100.0	174	17	AA98525 Hamster islet neog
2	174	100.0	175	19	AAW64790 INGAP protein frag
3	25	14.4	26	19	AAW64789 INGAP signal pepti
4	25	14.4	26	19	AAW55049 INGAP coding sequen
5	21	12.1	21	23	ABB79542 Hamster islet neog
6	15	8.6	15	23	ABB79543 Hamster islet neog
7	14	8.0	14	23	ABB79544 Hamster islet neog
8	14	8.0	14	23	ABB79545 Hamster islet neog
9	10	5.7	175	15	AAW34097 Mouse PAP. Mus mu
10	10	5.7	175	20	AAW95089 Reg-2 protein. Ra

11 10 5.7 175 21 AA198614
12 10 5.7 184 12 AA194797

Amino acid sequence
Rat pancreatitis a

ALIGNMENTS

RESULT 1

AA98525 standard; Protein; 174 AA.

AA98525;

18-APR-1997 (first entry)

Hamster islet neogenesis associated protein.

Hamster; islet neogenesis associated protein; INGAP; pancreas; endocrine; proliferation; pancreatic tissue; cellophane; duct epithelium; homology; differential display method; open reading frame; liver; adenocarcinoma; pancreatitis associated protein; lithostatine; pancreatic stone protein; beta-cell; regeneration; insulin; diabetes; mammal.

Cricetulus sp.

WO9626215-A1.

29-AUG-1996.

12-FEB-1996; 96WO-0501528.

07-NOV-1995; 95US-0006271.

22-FEB-1995; 95US-0401530.

(EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.

Duguid WP, Pittenger GL, Rafaeloff R, Rosenberg L;

Vinik AI;

WPI; 1996-402318/40.

N-PSDB; AAT36612.

Mammalian islet neogenesis associated protein - isolated by stimulating mammalian pancreas by wrapping in cellophane, for treatment of diabetes, etc

Claim 2; Page 26; 50pp; English.

This is the amino acid sequence of the hamster islet neogenesis associated protein (INGAP). The gene is isolated from pancreatic cells which are induced to proliferate upon wrapping pancreatic tissue in cellophane. Wrapping of the pancreas stimulate proliferation of new endocrine cells which appear from duct epithelium. The INGAP gene was isolated from a cDNA library constructed from mRNA purified from cellophane wrapped hamster pancreas using a differential display method to compare genes expressed in cellophane-wrapped and control pancreas. The gene contains an open reading frame which encodes a protein of 175 amino acids. The protein has structural homology to the pancreatitis associated protein (PAP)/HIP family of genes which is associated with pancreatic or liver adenocarcinoma, and to the Reg/PSP/lithostatine (PSP - pancreatic stone protein) family of gene which has been shown to stimulate pancreatic beta-cell growth and may be involved in pancreatic islet regeneration. The protein can be used to stimulate islet cell proliferation in (non-)insulin dependent diabetic mammals.

Sequence 174 AA;

Query Match 100.0%; Score 174; DB 17; Length 174;

Best local similarity 100.0%; Pred. No. 1.5e-174; Indels 0; Gaps 0;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MIPMTLCRMSWMLSCIMFLSWBGEESOKLPSSRTTCQGSVAAGSYCSILIPQW 60

Db 1 MLPMTLCRMSWMLLSCLMFLSMWVEGESQKLPSSRITCPQGSVAVGSYCYSLILIPQTW 60
 OY 61 SNAELSCQMHFSGHIAFLILSTGEITFFVSSLVKNLSITAVQYIWIGLHDSHGTLPNGSGWK 120
 Db 61 SNAELSCQMHFSGHIAFLILSTGEITFFVSSLVKNLSITAVQYIWIGLHDSHGTLPNGSGWK 120
 OY 121 WSSSNVLTFFYNMERNPSTIAADRGYCAVLQKSGFQKMDPNCENELPYICKFKY 174
 Db 121 WSSSNVLTFFYNMERNPSTIAADRGYCAVLQKSGFQKMDPNCENELPYICKFKY 174

RESULT 2

AAW64790
 ID AAW64790 standard; Protein: 175 AA.

XX AAW64790;

DT 18-NOV-1998 (first entry)

DE INGAP protein fragment.

KW INGAP; islet neogenesis-associated protein; treatment; diabetes;
 host cell.

XX Unknown.

PN US5804421-A.

PD 08-SEP-1998.

PF 12-AUG-1997; 97US-0909725.

PR 12-AUG-1997; 97US-0909725.

PR 30-OCT-1996; 96US-0741096.

PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.

PI Barlow SW, Pittenger GL, Rafaeloff-Phail R, Vink AI;

XX WPI; 1998-505656/43.

PT Expression of islet neogenesis-associated protein - from recombinant
 construct lacking signal peptide, useful in the treatment of

PT diabetes

PS Claim 1; Column 19-20; 14pp; English.

XX This sequence represents INGAP, an islet neogenesis-associated protein.
 CC This sequence is used in the construction of a recombinant construct
 CC having a coding sequence lacking a signal sequence and which is operably
 CC linked to transcription and translation initiation sites. This construct
 CC in a host cell is useful for producing recombinant mature INGAP, which
 CC is useful in the treatment of diabetes. High levels of INGAP expression
 CC can be achieved in bacterial and eukaryotic cells by removing the signal
 CC peptide as it is possibly toxic to cells.

XX Sequence 175 AA:

Query Match 100.0%; Score 174; DB 19; Length 175;

Best Local Similarity 100.0%; Pred. No. 1.5e-174; Mismatches 0; Indels 0; Gaps 0;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPMTLCRMSWMLLSCLMFLSMWVEGESQKLPSSRITCPQGSVAVGSYCYSLILIPQTW 60

Db 2 MLPMTLCRMSWMLLSCLMFLSMWVEGESQKLPSSRITCPQGSVAVGSYCYSLILIPQTW 61

OY 61 SNAELSCQMHFSGHIAFLILSTGEITFFVSSLVKNLSITAVQYIWIGLHDSHGTLPNGSGWK 120

Db 62 SNAELSCQMHFSGHIAFLILSTGEITFFVSSLVKNLSITAVQYIWIGLHDSHGTLPNGSGWK 121

OY 121 WSSSNVLTFFYNMERNPSTIAADRGYCAVLQKSGFQKMDPNCENELPYICKFKY 174

Db 122 WSSSNVLTFFYNMERNPSTIAADRGYCAVLQKSGFQKMDPNCENELPYICKFKY 175

RESULT 3
 AAW64789
 ID AAW64789 standard; Protein: 26 AA.

XX AAW64789;

DT 18-NOV-1998 (first entry)

DE INGAP signal peptide.

KW INGAP; islet neogenesis-associated protein; treatment; diabetes;
 host cell.

XX Unknown.

PN US5804421-A.

PD 08-SEP-1998.

PF 12-AUG-1997; 97US-0909725.

PR 12-AUG-1997; 97US-0909725.

PR 30-OCT-1996; 96US-0741096.

PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.

PI Barlow SW, Pittenger GL, Rafaeloff-Phail R, Vink AI;

XX WPI; 1998-505656/43.

DR N-PSDB; AAW64619.

PT Expression of islet neogenesis-associated protein - from recombinant
 construct lacking signal peptide, useful in the treatment of

PT diabetes

PS Example 1; Column 17-20; 14pp; English.

XX This cDNA sequence is the signal peptide of INGAP, an islet
 CC neogenesis-associated protein. This sequence is removed during the
 CC construction of a recombinant construct which has a coding
 CC sequence lacking a signal sequence and which is operably linked to
 CC transcription and translation initiation sites. This construct in a host
 CC cell is useful for producing recombinant mature INGAP, which is useful in
 CC the treatment of diabetes. High levels of INGAP expression can be
 CC achieved in bacterial and eukaryotic cells by removing the signal peptide
 CC as it is possibly toxic to cells.

XX Sequence 26 AA:

Query Match 14.4%; Score 25; DB 19; Length 26;

Best Local Similarity 100.0%; Pred. No. 8.7e-19; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MLPMTLCRMSWMLLSCLMFLSMWVEG 25

Db 2 MLPMTLCRMSWMLLSCLMFLSMWVEG 26

RESULT 4

AAW55049
 ID AAW55049 standard; Peptide: 26 AA.

XX AAW55049;

DT 25-SEP-1998 (first entry)

DE INGAP coding sequence signal peptide.

KW INGAP; pancreas; Iliotropin; islets of Langerhans; diabetes mellitus.

XX Mammalia.


```

XX PN WO9818913-A1.
XX PD 07-MAY-1998.
XX PF 30-OCT-1997; 97WO-US19415.
XX PR 30-OCT-1996; 96US-0741096.
XX PA (EVIR-) EASTERN VIRGINIA MEDICAL SCHOOL.
XX PI Barlow SM, Piltenger GI, Rataeloff R, Vinik AI;
XX DR WPI; 1998-272209/24.
XX DR N-PSDB; AAV30281.
XX PT .Expressing high levels of INGP using recombinant constructs -
XX PT peptide removed, useful for INGP production e.g. to treat diabetes
XX PS Claim 2; Page 5; 22pp; English.
XX CC The INGP signal peptide and the 5' UTR were excluded from a recombinant
XX CC construct for expressing INGP activity containing a nucleotide sequence
XX CC encoding amino acids 27-175 of INGP operably linked to a transcription
XX CC initiation site and a translational initiation site. The construct can
XX CC be used to produce biologically active INGP, by culturing the
XX CC transformed host cells. INGP is found within a pancreatic extract
XX CC called iliotropin and is known to be responsible for stimulating cell
XX CC regeneration of the pancreatic islets of Langerhans. The INGP produced
XX CC is useful in treatments to regenerate the islets of Langerhans to prevent
XX CC or ameliorate the symptoms of diabetes mellitus. Previous methods have
XX CC produced only low yields of INGP, possibly because the INGP signal
XX CC sequence is toxic to bacteria.
XX SQ Sequence 26 AA;
XX
XX Query Match 14.4%; Score 25; DB 19; Length 26;
XX Best Local Similarity 100.0%; Pred. No. 8,7e-19;
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MLPMPTLCRMSMMLSLCMLFSLWVEG 25
XX DB 2 MLPMPTLCRMSMMLSLCMLFSLWVEG 26
XX
XX RESULT 5
XX ABB79542
XX ID ABB79542 standard; Peptide; 21 AA.
XX AC ABB79542;
XX DX 01-OCT-2002 (first entry)
XX DE Hamster islet neogenesis associated protein (INGAP) immunogen.
XX KM Islet neogenesis associated protein; INGP; immunogen; hamster;
XX KM pancreas; diabetes; immunoassay.
XX OS Cricetus sp.
XX PN WO200256028-A2.
XX PD 18-JUL-2002.
XX PF 08-JAN-2002; 2002WO-US00071.
XX PR 09-JAN-2001; 2001US-260210P.
XX PR 07-JAN-2002; 2002US-0036418.
XX PA (GMPE-) GMP ENDOTHERAPETICS INC.
XX PI Vinik AI, Taylor-Fishwick D;

```

```

XX DR WPI; 2002-557841/59.
XX PT Assaying islet neogenesis associated protein (INGAP) for treating
XX PT diabetes types I and II, comprises determining the amount of labeled
XX PT INGP molecule bound to antibodies or to a solid support comprising the
XX PT bound antibodies
XX PS Claim 1; Page 12; 29pp; English.
XX CC The present sequence is a peptide immunogen corresponding to amino
XX CC acid residues 20-40 of full-length hamster islet neogenesis
XX CC associated protein (INGAP). The invention provides methods for
XX CC assaying INGP in a test sample. In a competitive binding assay,
XX CC antibodies which specifically bind to the INGP immunogen are
XX CC contacted with a test sample which may contain INGP protein, and a
XX CC labeled INGP molecule, e.g. a fusion protein comprising INGP
XX CC protein and a marker protein. The amount of labeled INGP
XX CC molecule bound to the antibodies is determined. This amount is
XX CC inversely related to INGP protein in the test sample. Antibodies
XX CC raised against different INGP immunogens (see ABB79543-45) and
XX CC their subfragments may also be used. They may be monoclonal or
XX CC polyclonal, may be bound to a solid support, and do not specifically
XX CC bind to other portions of the INGP protein or to other human
XX CC proteins. The method can be used to determine the amount of INGP
XX CC e.g. in culture media or biological tissues and fluids. The
XX CC ability to assay INGP will facilitate the full exploitation of
XX CC this protein for fighting human disease, such as diabetes types I
XX CC and II.
XX SQ Sequence 21 AA;
XX
XX Query Match 12.1%; Score 21; DB 23; Length 21;
XX Best Local Similarity 100.0%; Pred. No. 1.1e-14;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 19 FLSWVEGESQKRLPSSRITC 39
XX DB 1 FLSWVEGESQKRLPSSRITC 21
XX
XX RESULT 6
XX ABB79543
XX ID ABB79543 standard; Peptide; 15 AA.
XX AC ABB79543;
XX DX 01-OCT-2002 (first entry)
XX DE Hamster islet neogenesis associated protein (INGAP) immunogen.
XX KM Islet neogenesis associated protein; INGP; immunogen; hamster;
XX KM pancreas; diabetes; immunoassay.
XX OS Cricetus sp.
XX PN WO200256028-A2.
XX PD 18-JUL-2002.
XX PF 08-JAN-2002; 2002WO-US00071.
XX PR 09-JAN-2001; 2001US-260210P.
XX PR 07-JAN-2002; 2002US-0036418.
XX PA (GMPE-) GMP ENDOTHERAPETICS INC.
XX PI Vinik AI, Taylor-Fishwick D;
XX DR WPI; 2002-557841/59.
XX PT Assaying islet neogenesis associated protein (INGAP) for treating
XX PT diabetes types I and II, comprises determining the amount of labeled

```

PT INGP molecule bound to antibodies or to a solid support comprising the
 CC bound antibodies
 XX
 PS Claim 24; Page 14; 29pp; English.

XX The present sequence is a peptide immunogen corresponding to amino
 CC acid residues 104-118 of full-length hamster islet neogenesis
 CC associated protein (INGAP). The invention provides methods for
 CC assaying INGP in a test sample. In a competitive binding assay,
 CC antibodies which specifically bind to the INGP immunogen are
 CC contacted with a test sample which may contain INGP protein, and a
 CC labelled INGP molecule, e.g. a fusion protein comprising INGP
 CC protein and a marker protein. The amount of labelled INGP
 CC molecule bound to the antibodies is determined. This amount is
 CC inversely related to INGP protein in the test sample. Antibodies
 CC raised against different INGP immunogens (see ABB79542-45) and
 CC their subfragments may also be used. They may be monoclonal or
 CC polyclonal, may be bound to a solid support, and do not specifically
 CC bind to other portions of the INGP protein or to other human
 CC proteins. The method can be used to determine the amount of INGP
 CC e.g. in culture media or biological tissues and fluids. The
 CC ability to assay INGP will facilitate the full exploitation of
 CC this protein for fighting human disease, such as diabetes types I
 CC and II.
 XX
 SQ Sequence 15 AA;

Query Match 8.6%; Score 15; DB 23; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.6e-08;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 103 IGLHDPHSGTLPNGS 117
 ID 1 IGLHDPHSGTLPNGS 15

RESULT 7
 ABB79544
 ID ABB79544 standard; Peptide; 14 AA.
 XX
 AC ABB79544;

DT 01-OCT-2002 (first entry)
 XX

DE Hamster islet neogenesis associated protein (INGAP) immunogen.

XX Islet neogenesis associated protein; INGP; immunogen; hamster;
 KW pancreas; diabetes; immunoassay.
 XX

OS Cricetus sp.
 XX

PN WO200256028-A2.
 XX

PD 18-JUL-2002.
 XX

PF 08-JAN-2002; 2002WO-US00071.
 XX

PR 09-JAN-2001; 2001US-260210P.
 XX

PR 07-JAN-2002; 2002US-0036418.
 XX

PA (GMPE-) GMP ENDOTHERAPEUTICS INC.
 XX

PI Vinik AI, Taylor-Fishwick D;
 XX

DR WPI; 2002-557841/59.
 XX

PT Assaying islet neogenesis associated protein (INGAP) for treating
 PT diabetes types I and II, comprises determining the amount of labeled
 PT INGP molecule bound to antibodies or to a solid support comprising the
 PT bound antibodies
 XX

PS Claim 24; Page 14; 29pp; English.
 XX

CC The present sequence is a peptide immunogen corresponding to amino
 CC acid residues 139-152 of full-length hamster islet neogenesis
 CC associated protein (INGAP). The invention provides methods for
 CC assaying INGP in a test sample. In a competitive binding assay,
 CC antibodies which specifically bind to the INGP immunogen are
 CC contacted with a test sample which may contain INGP protein, and a
 CC labelled INGP molecule, e.g. a fusion protein comprising INGP
 CC protein and a marker protein. The amount of labelled INGP
 CC molecule bound to the antibodies is determined. This amount is
 CC inversely related to INGP protein in the test sample. Antibodies
 CC raised against different INGP immunogens (see ABB79542-45) and
 CC their subfragments may also be used. They may be monoclonal or
 CC polyclonal, may be bound to a solid support, or do not specifically
 CC bind to other portions of the INGP protein or to other human
 CC proteins. The method can be used to determine the amount of INGP
 CC e.g. in culture media or biological tissues and fluids. The
 CC ability to assay INGP will facilitate the full exploitation of
 CC this protein for fighting human disease, such as diabetes types I
 CC and II.
 XX

SQ Sequence 14 AA;
 Query Match 8.0%; Score 14; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 IADRGYCAVLSQK 151
 ID 1 IADRGYCAVLSQK 14

RESULT 8
 ABB79545
 ID ABB79545 standard; Peptide; 14 AA.
 XX
 AC ABB79545;

DT 01-OCT-2002 (first entry)
 XX

DE Hamster islet neogenesis associated protein (INGAP) immunogen.

XX Islet neogenesis associated protein; INGP; immunogen; hamster;
 KW pancreas; diabetes; immunoassay.
 XX

OS Cricetus sp.
 XX

PN WO200256028-A2.
 XX

PD 18-JUL-2002.
 XX

PF 08-JAN-2002; 2002WO-US00071.
 XX

PR 09-JAN-2001; 2001US-260210P.
 XX

PR 07-JAN-2002; 2002US-0036418.
 XX

PA (GMPE-) GMP ENDOTHERAPEUTICS INC.
 XX

PI Vinik AI, Taylor-Fishwick D;
 XX

DR WPI; 2002-557841/59.
 XX

PT Assaying islet neogenesis associated protein (INGAP) for treating
 PT diabetes types I and II, comprises determining the amount of labeled
 PT INGP molecule bound to antibodies or to a solid support comprising the
 PT bound antibodies
 XX

PS Claim 24; Page 14; 29pp; English.
 XX

CC The present sequence is a peptide immunogen corresponding to amino
 CC acid residues 131-164 of full-length hamster islet neogenesis
 CC associated protein (INGAP). The invention provides methods for
 CC assaying INGP in a test sample. In a competitive binding assay,
 CC antibodies which specifically bind to the INGP immunogen are

CC contacted with a test sample which may contain INGP protein, and a
 CC labelled INGP molecule. e.g. a fusion protein comprising INGP
 CC protein and a marker protein. The amount of labelled INGP
 CC molecule bound to the antibodies is determined. This amount is
 CC inversely related to INGP protein in the test sample. Antibodies
 CC raised against different INGP immunogens (see AB87942-45) and
 CC their subfragments may also be used. They may be monoclonal or
 CC polyclonal, may be bound to a solid support, and do not specifically
 CC bind to other portions of the INGP protein or to other human
 CC proteins. The method can be used to determine the amount of INGP
 CC e.g. in culture media or biological tissues and fluids. The
 CC ability to assay INGP will facilitate the full exploitation of
 CC this protein for fighting human disease, such as diabetes types I
 CC and II.

CC
 XX
 SQ Sequence 14 AA;

Query Match 8.0%; Score 14; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : 150 QKSGFQKWRDENCE 163
 DB 1 QKSGFQKWRDENCE 14

RESULT 9

AAR54097
 ID AAR54097 standard; Protein; 175 AA.

XX AAR54097;

XX 01-FEB-1995 (first entry)

XX Mouse PAP.

XX Pancreatitis-Associated Protein; PAP; mouse; human; bacteria;
 aggregation; antibacterial; primer; PCR.

XX Mus musculus.

XX JP06135998-A.

XX 17-MAY-1994.

XX 22-OCT-1992; 92UP-0284765.

XX 22-OCT-1992; 92UP-0284765.

XX (SHIO) SHIONOGI & CO LTD.

XX WPI; 1994-197103/24.

XX N-PSDB; AAO64171.

XX Human and mouse pancreatitis-associated protein (PAP) - useful
 for prep. of proteolaceous antibacterial agent

XX Claim 1-6; Page 5-6; 7pp; Japanese.

XX PAP DNA has a high bacteria-aggregating activity and is useful for
 CC the prep. of PAP which can act as a proteolaceous antibacterial
 CC agent. Total RNA was isolated from mouse. It was hybridised with a
 CC modified salmon spermatozoa DNA and known rat PAP cDNA as a probe.
 CC Two primers are given in AAO64173-74.

XX SQ- Sequence 175 AA;

Query Match 5.7%; Score 10; DB 15; Length 175;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MSMMLLSCLM 18
 XXXXXXXXXXXXXXX

DB 10 MSMMLLSCLM 19

RESULT 10

AAM95089
 ID AAM95089 standard; Protein; 175 AA.

XX AAM95089;

XX 20-MAY-1999 (first entry)

XX Reg-2 protein.

XX Reg-2; Schwann cell mitogen; repair; regenerate; neuronal cell; tissue;
 glial growth factor; neuroglin.

XX Rattus sp.

XX GB2329335-A.

XX 24-MAR-1999.

XX 16-SEP-1998; 98GB-0020193.

XX 17-SEP-1997; 97GB-0019796.

XX (MEDIC-) MEDICAL RES COUNCIL.

XX Hunt SP, Livezey EJ;

XX WPI; 1999-156299/14.

XX N-PSDB; AAX26126.

XX Use of a protein (Reg-2) to manufacture a Schwann cell mitogen, -- to
 repair and/or regenerate neuronal cells or tissue, either in vivo,
 or in vitro and then introduced into subject

XX Claim 1; Page 24; 33pp; English.

XX The invention relates to the use of a protein (Reg-2) or its variant,
 CC derivative or homologue to manufacture a Schwann cell mitogen. Reg-2 is
 CC used to repair and/or regenerate neuronal cells or tissue. Neuronal cells
 CC or tissue may be repaired and/or regenerated either in vivo, or in vitro
 CC and then introduced into a subject. Reg-2 unlike known Schwann cell
 CC mitogens e.g. glial growth factors/neuregulins, are upregulated during
 CC regeneration. The present sequence represents the Reg-2 protein.

XX SQ Sequence 175 AA;

Query Match 5.7%; Score 10; DB 20; Length 175;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MSMMLLSCLM 18
 DB 10 MSMMLLSCLM 19

RESULT 11

AAB18614
 ID AAB18614 standard; Protein; 175 AA.

XX AAB18614;

XX 15-JAN-2001 (first entry)

XX Amino acid sequence of a rat Reg-2 polypeptide.

XX Schwann cell mitogen; Reg-2; neuronal cell regeneration; motor neuron;
 neuron-glial interaction.

XX Rattus sp.

XX

XX

XX

XX

XX

```

PN GB2347931-A.
XX
XX 20-SEP-2000.
XX
XX 02-FEB-2000; 2000GB-0002424.
XX
XX 17-SEP-1997; 97GB-0019796.
XX 16-SEP-1998; 98GB-0020193.
XX
XX (MED1-) MEDICAL RES COUNCIL.
XX
XX Livesey FJ, Hunt SP;
XX
XX WPI; 2000-567204/53.
XX
XX N-PSDB; AAA75486.
XX
XX New Schwann cell mitogen (known as Reg-2), useful for repair and
XX regeneration of neuronal cells and tissue, is upregulated during
XX neuronal regeneration -
XX
XX Claim 2; Page 24; 32pp; English.
XX
XX The present sequence represents a Schwann cell mitogen, known as Reg-2.
XX Reg-2 can be upregulated during regeneration of neuronal cells and
XX tissue. Reg-2 is an essential component in neuron-glia interaction
XX that underlies development and regeneration of mammalian motor
XX neurons. It is a 16 kDa protein. Reg-2 is used to affect development
XX of neuronal cells and tissue, especially for promoting their repair
XX and regeneration, particularly of motor cells in adult humans.
XX
XX
SQ Sequence 175 AA:
Query Match 5.7%; Score 10; DB 21; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 MSWMLISCLM 18
DB 10 MSWMLISCLM 19

RESULT 12
AAR14797
ID AAR14797 standard; Protein; 184 AA.
XX
XX AAR14797;
XX
XX 29-JAN-1992 (first entry)
XX
XX Rat pancreatitis associated protein A1.
XX
XX hPAP; pancreas; imaging.
XX
XX Rattus.
XX
XX
XX Key Location/Qualifiers
XX FH 1..26
XX FT 27..184
XX FT /label= mature PAP
XX
XX WO9116428-A.
XX
XX 31-OCT-1991.
XX
XX 18-APR-1991; 91WO-FR00323.
XX
XX 20-APR-1990; 90FR-0005062.
XX
XX (INRM ) INSERM INST NAT SANTE.
XX
XX Iovanna JL, Keim V, Dagron JC;
XX
XX WPI; 1991-339816/46.

```

```

DR N-PSDB; AAQ14621.
XX
XX cDNA fragment of human pancreatitis associated protein -
XX produced by genetic engineering, and the corresponding antibody,
XX for use in the diagnosis of pancreatitis
XX
XX Claim 16; Page 34; 49pp; French.
XX
XX The cDNA fragment SI encoding the rat PAP was isolated from a rat
XX pancreatic cDNA library using antibodies against rat PAP.
XX
XX
XX Sequence 184 AA:
Query Match 5.7%; Score 10; DB 12; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 MSWMLISCLM 18
DB 10 MSWMLISCLM 19

```

Search completed: April 16, 2003, 10:49:28
Job time : 37 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:48:26 ; Search time 17 seconds

(Without alignments)
983.964 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 174
1 MLPMTLCRMSMMLSLCLMFL.....QKWRDPCENELPYICKEKY 174

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size: 10

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	10	5.7	175	2 A41719	pancreatic stone p
2	10	5.7	175	2 S29822	pancreatitis-assoc

ALIGNMENTS

RESULT 1
A41719
pancreatic stone protein 2 precursor - rat
N:Alternate names: pancreatitis-associated protein; regenerating protein 2
C/Species: Rattus norvegicus (Norway rat)
C/Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 20-Jun-2000
C/Accession: A37456; A59313; I51899; JCI257; A41719
R/Dusetti, N.J.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
J. Biol. Chem. 268, 14470-14475, 1993
A/Title: Structural organization of the gene encoding the rat pancreatitis-associated pr
on domain-containing genes.
A/Reference number: A37456; MUID:93300847; PMID:8314803
A/Accession: A37456
A/Molecule type: DNA
A/Residues: 1-175 <DUS1>
A/Cross-references: GB:I07127; NID:9349550
A/Note: only intron/exon boundaries are shown, exon I and the beginning of exon II are c
enson of the open reading frame to an ATG codon in exon I is shown in accession A59313
R/Dusetti, N.J.; Frigerio, J.M.; Keim, V.; Dagorn, J.C.; Iovanna, J.L.
submitted to Genbank, August 1993
A/Reference number: A59313

A/Accession: A59313
A/Status: not compared with conceptual translation
A/Molecule type: DNA
A/Residues: 'MMRVK', 1-175 <DUS2>
A/Cross-references: GB:I07127; NID:9349550; PIDN:AAA41805.1; PID:9349551
A/Note: an incorrect initiation codon was used
R/Iovanna, J.L.; Keim, V.; Bosshard, A.; Orelle, B.; Frigerio, J.M.; Dusetti, N.; Dag
Am. J. Physiol. 265, G611-G618, 1993
A/Title: PAP, a pancreatic secretory protein induced during acute pancreatitis, is ex
A/Reference number: I51899; MUID:94056762; PMID:8238345
A/Accession: I51899
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-175 <IOV1>
A/Cross-references: GB:98049; NID:9393210; PIDN:AAA16341.1; PID:9393211
A/Note: in Genbank entry RAMPAPC release 113.0, the source is designated as Rattus r
R/Kamimura, T.; West, C.; Beutler, E.
Gene 118, 299-300, 1992
A/Title: Sequence of a cDNA clone encoding a rat Reg-2 protein.
A/Reference number: JCI257; MUID:92380521; PMID:1511905
A/Accession: JCI257
A/Molecule type: mRNA
A/Residues: 1-6, 'S', 8-175 <KAM>
A/Cross-references: GB:843715; NID:9254694; PIDN:AA823103.1; PID:9254695
R/Iovanna, J.; Orelle, B.; Keim, V.; Dagorn, J.C.
J. Biol. Chem. 266, 24664-24669, 1991
A/Title: Messenger RNA sequence and expression of rat pancreatitis-associated protein
A/Reference number: A41719; MUID:92105133; PMID:1722211
A/Accession: A41719
A/Molecule type: mRNA
A/Residues: 1-175 <IOV2>
A/Cross-references: GB:M55149; NID:9206030; PIDN:AAA11807.1; PID:9206031
A/Note: the amino-terminal residue of the mature protein was identified as Glu
C/Genetics:
A/Gene: pap
A/Introns: 26/1; 65/3; 111/3; 154/1
A/Note: the first intron occurs before the initiator codon
C/Superfamily: tetraneurin; C-type lectin homology
C/Keywords: lectin; pancreas
F.1-26/Domain: signal sequence #status predicted <SIG>
F.1-27-175/Product: pancreatitis-associated protein #status experimental <MAT>
F.40-171/Domain: C-type lectin homology <LCH>
F.40-51,68-171,146-163/Disulfide bonds: #status predicted

Query Match 5.7%; Score 10; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 MSMMLSLCLM 18
DB 10 MSMMLSLCLM 19

RESULT 2
S29822
pancreatitis-associated protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C/Accession: S29822
R/Itch, T.; Teraoka, H.
Biochim. Biophys. Acta 1172, 184-186, 1993
A/Title: Cloning and tissue-specific expression of cDNAs for the human and mouse homo
A/Reference number: S29821; MUID:93176807; PMID:7679928
A/Accession: S29822
A/Molecule type: mRNA
A/Status: preliminary
A/Residues: 1-175 <ITM>
A/Cross-references: GB:D13509; NID:9286106; PIDN:BA02727.1; PID:9286107
C/Superfamily: tetraneurin; C-type lectin homology
F.40-171/Domain: C-type lectin homology <LCH>

Query Match 5.7%; Score 10; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.0085;

Matches	10;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	9	MSMMLISCIM	18						
Db	10	MSMMLISCIM	19						

Search completed: April 16, 2003, 10:50:48
Job time : 18 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Comugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:47:30 ; Search time 12 seconds

(Without alignments)
601.407 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 1 MLPMTLCRMSWMLSLCLMFL.....QKWRDPCENELPYICKFV 174

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 10

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	174	100.0	175	1	PBQ_HUMAN
2	10	5.7	174	1	PAP3_MOUSE
3	10	5.7	175	1	PAP1_MOUSE
4	10	5.7	175	1	PAP1_RAT

ALIGNMENTS

RESULT 1
PBQ_HUMAN STANDARD: PRT: 175 AA.
AC 092778; P70109;
DT 15-JUL-1998 (Rel. 36, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatic beta cell growth factor precursor (Islet neogenesis DE associated protein).
GN INGP.
OS Homo sapiens (Human), and
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606, 10036;
RN [1]
RP SEQUENCE FROM N.A., AND SYNTHESIS OF 104-118.
RC STRAIN-Lake View Golden; TISSUE-Pancreas;
RX MEDLINE=97296198; PubMed=9151782;
RA Rafaeiloff R., Pittenger G.L., Barlow S.W., Qin X.F., Yan B.,
RA Rosenberg L., Duguid W.P., Vink A.L.;
RT "Cloning and sequencing of the pancreatic islet neogenesis associated
RT protein (INGAP) gene and its expression in islet neogenesis in
RT hamsters.";

RL J. Clin. Invest. 99:2100-2109(1992).
CC -FUNCTION: CONSTITUENT OF ILIOTROPIN, WHICH IS A PARTIALLY PURIFIED
CC PREPARATION OF CELLOPHANE WRAPPING (CW) PANCREATA. CAPABLE OF
CC INITIATING DUCT CELL PROLIFERATION, A PREREQUISITE FOR ISLET
CC NEOGENESIS.
CC -SUBCELLULAR LOCATION: Secreted (By similarity).
CC -TISSUE SPECIFICITY: EXPRESSED ONLY IN CW ANIMALS PANCREAS AND TO A
CC LESSER EXTENT IN DUODENUM. IN PANCREAS IT IS FOUND IN ACINAR
CC CELLS, BUT NOT IN ISLETS.
CC -INDUCTION: FOUND 1 AND 2 DAYS AFTER CELLOPHANE WRAPPING, ABSENT BY
CC THE 6TH DAY. THIS PERIOD COINCIDES WITH ISLET NEOGENESIS.
CC -SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-2 OR MET-5 IS THE
CC INITIATOR.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U41737; AAB86497.1; ALT_INT.
DR EMBL: U41738; AAB16754.1; ALT_INT.
DR HSPR: P05451.1; IODD.
DR InterPro: IPR000282; CytoK_receptor_2.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR003990; PancreatIs_ac.
DR Pfam: PF00059; Lectin_cj_1.
DR PRINTS: PR01504; PNCREATITSAP.
DR SMART: SM00034; CLECT. 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; 1.
DR PROSITE: PS50041; C-TYPE LECTIN_2; 1.
KW Signal; Lectin.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 175 PANCREATIC BETA CELL GROWTH FACTOR.
FT DOMAIN 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA: 19940 MW: 3854368A35D17CE CRC64;
Query Match 100.0%; Score 174; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 7.5e-176;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MLPMTLCRMSWMLSLCLMFLSMVEGEESOKRUPSSRTICPOGSYAVGSYCSILLIPQW 60
DB 2 MLPMTLCRMSWMLSLCLMFLSMVEGEESOKRUPSSRTICPOGSYAVGSYCSILLIPQW 61
OY 61 SNAELSCQMHSGHIAFLITSTGETTFVSSLVKNSLTAYQIYIGLHDPHSGTLPNGSGMK 120
DB 62 SNAELSCQMHSGHIAFLITSTGETTFVSSLVKNSLTAYQIYIGLHDPHSGTLPNGSGMK 121
OY 121 MSSSNVLFYNNERNPSTADRGCAVLSOKSGQKMRDPCENELPYICKFV 174
DB 122 MSSSNVLFYNNERNPSTADRGCAVLSOKSGQKMRDPCENELPYICKFV 175
RESULT 2
PAP3_MOUSE STANDARD: PRT: 174 AA.
AC 009049;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 3 precursor (REG III-gamma).
GN PAP3 OR REG3G.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-Liver, and Pancreas;
RX MEDLINE-97208868; PubMed-9055810;
RA Narushima Y., Uno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.;
RT Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
RL gene 185:159-168(1997).
CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
CC BACTERIAL PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN THE SMALL
CC INTESTINE, MODERATELY IN COLON AND AT AN EXTREMELY LOW LEVEL IN
CC HEALTHY PANCREAS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D63361; BAA18930.1; -
DR EMBL: D63362; BAA18931.1; -
DR HSSP: P05451; ILIT.
DR MGD: MGI:109406; Reg3g.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR003990; Pancreatis_ac.
DR Pfam: PF00059; lectin_C; 1.
DR PRINTS: PR01504; PNCREATTISAP.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; FALSE_NEG.
DR PROSITE: PS00041; C-TYPE_LECTIN_2; 1.
DR SIGNAL: Lectin; Inflammatory response; Acute phase; Multigene family.
KW SIGNAL; 1
FT CHAIN 1 26 POTENTIAL.
FT DOMAIN 27 174 PANCREATTIS-ASSOCIATED PROTEIN 3.
FT DISULFID 38 172 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 170 BY SIMILARITY.
FT DISULFID 145 162 BY SIMILARITY.
SQ SEQUENCE 174 AA; 19307 MW; 5575E9E564DCEFC CRC64;

Query Match 5.7%; Score 10; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 MSWMLSCIM 18
DB 10 MSWMLSCIM 19

RESULT 3
PAP1_MOUSE
ID PAP1_MOUSE STANDARD; PRT; 175 AA.
AC P35230;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (REG III-beta).
DE PAP1 OR PAP OR REG3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid-10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE-Pancreas, and Small intestine;
RX MEDLINE-93176807; PubMed-7679928;
RA Itoh T., Teraoka H.;

```

```

RT "Cloning and tissue-specific expression of cDNAs for the human and
RT mouse homologues of rat pancreatitis-associated protein (PAP).";
RL Biochim. Biophys. Acta 1172:184-186(1993).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE-Pancreas;
RX MEDLINE-97208868; PubMed-9055810;
RA Narushima Y., Uno M., Nakagawara K.-I., Mori M., Miyashita H.,
RA Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
RA Okamoto H.;
RT Structure, chromosomal localization and expression of mouse genes
RT encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma.";
RL gene 185:159-168(1997).
CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
CC BACTERIAL PROLIFERATION.
CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
CC PANCREATIC ACINAR CELLS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN THE SMALL
CC INTESTINE, MODERATELY IN COLON AND AT AN EXTREMELY LOW LEVEL IN
CC HEALTHY PANCREAS.
CC -1- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF
CC PANCREATIC INFLAMMATION.
CC -1- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATTITIS.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D13509; BAA02727.1; -
DR EMBL: D63359; BAA18928.1; -
DR EMBL: D63360; BAA18929.1; -
DR PIR: S29822; S29822.
DR HSSP: P05451; ILIT.
DR MGD: MGI:97478; Pap.
DR InterPro: IPR001304; Lectin_C.
DR InterPro: IPR003990; Pancreatis_ac.
DR Pfam: PF00059; lectin_C; 1.
DR PRINTS: PR01504; PNCREATTISAP.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
DR PROSITE: PS00041; C-TYPE_LECTIN_2; 1.
DR SIGNAL: Lectin; Inflammatory response; Acute phase; Multigene family.
KW SIGNAL; 1
FT CHAIN 1 26 BY SIMILARITY.
FT DOMAIN 27 175 PANCREATTIS-ASSOCIATED PROTEIN 1.
FT DISULFID 38 173 C-TYPE LECTIN (LONG FORM).
FT DISULFID 40 51 BY SIMILARITY.
FT DISULFID 68 171 BY SIMILARITY.
FT DISULFID 146 163 BY SIMILARITY.
SQ SEQUENCE 175 AA; 19476 MW; 44B3101171E79775 CRC64;

Query Match 5.7%; Score 10; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 MSWMLSCIM 18
DB 10 MSWMLSCIM 19

RESULT 4
PAP1_RAT
ID PAP1_RAT STANDARD; PRT; 175 AA.
AC P25031; Q64231; Q64102;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pancreatitis-associated protein 1 precursor (Peptide 23) (REG-2).
DE PAP1 OR PAP OR REG2.
GN

```


OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-39.
 RC STRAIN-Sprague-Dawley; TISSUE-Pancreas;
 RX MEDLINE=92105133; PubMed=1722211;
 RA Iovanna J., Orelle B., Keim V., Dagorn J.-C.;
 RT Messenger RNA sequence and expression of rat pancreatitis-associated
 RT protein, a lectin-related protein overexpressed during acute
 RT experimental pancreatitis.";
 RL J. Biol. Chem. 266:2464-2466(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Intestine;
 RX MEDLINE=94056762; PubMed=8238345;
 RA Iovanna J.L., Keim V., Bosshard A., Orelle B., Frigerio J.M.,
 RA Dusetti N., Dagorn J.C.;
 RT "PAP, a pancreatic secretory protein induced during acute
 RT pancreatitis, is expressed in rat intestine.";
 RL Am. J. Physiol. 265:G611-G618(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Wistar; TISSUE-Liver;
 RX MEDLINE=93300847; PubMed=8314803;
 RA Dusetti N.J., Frigerio J.M., Keim V., Dagorn J.C., Iovanna J.;
 RT "Structural organization of the gene encoding the rat pancreatitis-
 RT associated protein. Analysis of its evolutionary history reveals an
 RT ancient divergence from the other carbohydrate-recognition domain-
 RT containing genes.";
 RL J. Biol. Chem. 268:14470-14475(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92380521; PubMed=1511905;
 RA Kamimura T., West C., Beutler E.;
 RT "Sequence of a cDNA clone encoding a rat Reg-2 protein.";
 RL Gene 118:299-300(1992).
 RN [5]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-Sprague-Dawley; TISSUE-Pituitary;
 RX MEDLINE=95203187; PubMed=7895644;
 RA Katsumata N., Chakraborty C., Myal Y., Schroeder I.C.,
 RA Murphy L.J., Shiu R.P., Friesen H.G.;
 RT "Molecular cloning and expression of peptide 23, a growth hormone-
 RT releasing hormone-inducible pituitary protein.";
 RL Endocrinology 136:1332-1339(1995).
 CC -1- FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF
 CC BACTERIAL PROLIFERATION.
 CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND IN THE APICAL REGION OF
 CC PANCREATIC ACINAR CELLS.
 CC -1- TISSUE SPECIFICITY: CONSTITUTIVELY EXPRESSED IN INTESTINE.
 CC -1- INDUCTION: APPEARS IN PANCREATIC JUICE AFTER INDUCTION OF
 CC PANCREATIC INFLAMMATION. SECRETED ALSO BY PITUITARY CELLS; THE
 CC SECRETION THERE IS STIMULATED BY GH-RELEASING HORMONE AND
 CC INHIBITED BY SOMATOSTATIN.
 CC -1- DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M55149; AAA1807.1; -
 DR EMBL: M98049; AAA16341.1; -
 DR EMBL: L07127; AAA1805.1; ALT_INT.
 DR EMBL: S45715; AAB2103.1; -
 DR EMBL: S77413; AAB3848.2; -
 DR PIR: A41719; A41719.

DR HSP: P05451; 10DD.
 DR InterPro: IPR001304; Lectin_C.
 DR InterPro: IPR003900; Pancreatis_ac.
 DR Pfam: PF00059; Lectin_c; 1.
 DR PRINTS: PR01504; PNCREATITISAP.
 DR SMART: SM00034; CLECT; 1.
 DR PROSITE: PS00615; C-TYPE_LLECTIN_1; 1.
 DR PROSITE: PS50041; C-TYPE_LLECTIN_2; 1.
 KW Signal; Lectin; Inflammatory response; Acute phase.
 FT SIGNAL 1 26
 FT CHAIN 27 175
 FT DOMAIN 38 173
 FT DISULFID 40 51
 FT DISULFID 68 171
 FT DISULFID 146 163
 FT CONFLICT 7 7
 FT CONFLICT 123 123
 SQ SEQUENCE 175 AA: 19617 MW: C43892BP31B0B525 CRC64;
 S -> S (IN REF. 4).
 F -> T (IN REF. 5).
 Query Match 5.7%; Score 10; DB 1; Length 175;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: April 16, 2003, 10:49:46
 Job time : 12 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:47:51 ; Search time 30 Seconds
(without alignments)
1195.073 Million cell updates/sec

Title: US-08-401-530-2

Perfect score: 174
Sequence: 1 MIPMTLCRMSNMLSCMLF.....QKMFNCENELPYCKFKV 174

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 segs, 206047115 residues

Word size : 10

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	40.2	138	11	09QYF7 mesocricetu
2	11	6.3	98	11	09QYF8 mus musculi
3	11	6.3	175	11	09JMH1 mus musculi
4	11	6.3	175	11	09QUS9 mus musculi

ALIGNMENTS

RESULT 1
09QYF7 PRELIMINARY: PRT: 138 AA.
AC 09QYF7:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE Islet neogenesis associated protein (Fragment).
GN INGP.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231736; PubMed=10767532;
RA Abe M., Nata K., Akiyama T., Ito S., Takasawa S., Okamoto H.,
RA Tomioka-Kunagai T., Ito S., Takasawa S., Okamoto H.,
RT Identification of a novel Reg family gene, Reg III delta, and mapping
RT of all three types of Reg family gene in a 75 kilobase mouse genomic
RT region."
RL Gene 246:111-122(2000).
DR EMBL: AB035211; BAA88566.1; -.
DR HSSP: P05451; 10DD.
DR InterPro: IPR000282; CytoK_receptor_2.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C_1.
DR SMART: SM00034; CLECT_1.
DR PROSITE: PS00615; C_Type_Lectin_1; 1.
DR PROSITE: PS50041; C_Type_Lectin_2; 1.
FT NON_TER 1
SQ SEQUENCE 138 AA; 15585 MW; 4E3BB8AAAD1B524 CRC64;

Query Match 40.2%; Score 70; DB 11; Length 138;
Best Local Similarity 100.0%; Pred. No. 8.8e-68;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 37 ITCPOGSVAVGSCYCSLILIPOTWSNALS COMFSGHIAFLSTGRTFVSSLVKNSLT 96
DB 1 ITCPOGSVAVGSCYCSLILIPOTWSNALS COMFSGHIAFLSTGRTFVSSLVKNSLT 60
QY 97 AYOYTWIGLH 106
DB 61 AYOYTWIGLH 70

RESULT 2
09QYF8 PRELIMINARY: PRT: 98 AA.
AC 09QYF8:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Reg III delta (Fragment).
GN INGP OR REG3A OR REG3D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20231736; PubMed=10767532;
RA Abe M., Nata K., Akiyama T., Shervani N.J., Kobayashi S.,
RA Tomioka-Kunagai T., Ito S., Takasawa S., Okamoto H.,
RT Identification of a novel Reg family gene, Reg III delta, and mapping
RT of all three types of Reg family gene in a 75 kilobase mouse genomic
RT region."
RL Gene 246:111-122(2000).
DR EMBL: AB035203; BAA88562.1; -.
DR HSSP: P05451; 1LIT.
DR MGD: MGI:109408; Reg3a.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_C_1.
DR PROSITE: PS50041; C_Type_Lectin_2; 1.
FT NON_TER 98
SQ SEQUENCE 98 AA; 11248 MW; 871BCC93FAD00595 CRC64;
Query Match 6.3%; Score 11; DB 11; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVSSLVKNLSLT 96
DB 77 FVSSLVKNLSLT 87

RESULT 3

090JMH1 PRELIMINARY; PRT; 175 AA.

AC 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE INGAR related protein.
GN INGARPR OR INGARPR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BDF-1; TISSUE=DUDENDUM;
RX MEDLINE=20033449; PubMed=10564727;
RA Sasakura K., Yamaoka T., Moritani M., Yoshimoto K., Kuroda Y.,
RA Itakura M.;
RT "Molecular cloning and tissue-specific expression of a new member of
RT the regenerating protein family, islet neogenesis-associated protein-
RT related protein."
RL Blochm. Biophys. Acta 1500:142-146(2000).
DR EMBL: AB028625; BAA92141.1; -.
DR HSSP: P05451; IQDD.
DR MGD: MGI:1353426; Ingaprp.
DR Interpro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
SQ SEQUENCE 175 AA; 20021 MM; 0A92F6112BC6B53 CRC64;

Query Match 6.3%; Score 11; DB 11; Length 175;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVSSLVKNLSLT 96
DB 87 FVSSLVKNLSLT 97

RESULT 4
090US9 PRELIMINARY; PRT; 175 AA.
AC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE REG III delta precursor (Islet neogenesis associated protein-related
DE protein).
GN INGARPR OR REG3D.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Abe M., Nata K., Tomioka-Kumagai T., Takawa S., Ito S., Okamoto H.;
RT "Identification of a novel Reg family gene, Reg III delta, and mapping
RT of all three types of Reg family genes in 75-Kilobase mouse genomic
RT region."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Felschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Mashio T.,
RA Sakai K., Okido T., Furuno M., Kono H., Baldarelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustafson S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink U.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AB035204; BAA8564.1; -.
DR EMBL: AB035205; BAA8565.1; -.
DR EMBL: AK019033; BAB31518.1; -.
DR HSSP: P05451; IQDD.
DR MGD: MGI:1353426; Ingaprp.
DR Interpro: IPR001304; Lectin_C.
DR Pfam: PF00059; lectin_c; 1.
DR PRINTS: PR01504; PNCREPTISAP.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE: PS50041; C_TYPE_LLECTIN_2; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 175 AA; 20037 MM; 0A8BD67512BC6B53 CRC64;

Query Match 6.3%; Score 11; DB 11; Length 175;

Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 FVSSLVKNLSLT 96
DB 87 FVSSLVKNLSLT 97

Search completed: April 16, 2003, 10:50:24
Job time : 30 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:48:51 ; Search time 15 Seconds
(without alignments)
341.306 Million cell updates/sec

Title: US-08-401-530-2

Sequence: 174
1 MPMPTLCRMSMLSCMLFL.....QKWRDNCENELPYICKFY 174

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 10

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/1aa/PCUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	174	100.0	174	2	US-08-401-530A-2
2	174	100.0	174	2	US-08-709-662-2
3	174	100.0	175	1	US-08-909-725-6
4	25	14.4	26	1	US-08-909-725-5
5	11	6.3	175	2	US-08-401-530A-3
6	11	6.3	175	2	US-08-709-662-3
7	10	5.7	184	1	US-07-778-156-2
8	10	5.7	184	2	US-08-422-166-2

ALIGNMENTS

RESULT 1
US-08-401-530A-2
; Sequence 2, Application US/08401530A
; Patent No. 5834590
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Pittenger, Gary L.
; APPLICANT: Rafaeloff, Ronit
; APPLICANT: Rosenberg, Lawrence
; APPLICANT: Duguid, William P.
; TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:

ADDRESS: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.48743
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-401-530A-2
Query Match 100.0%; Score 174; DB 2; Length 174;
Best local similarity 100.0%; Pred. No. 3.1e-171;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPMPTLCRMSMLSCMLFLSWVEGEESQKLPSSRTICPGGSVAYGSCYSLILPQTW 60
DB 1 MPMPTLCRMSMLSCMLFLSWVEGEESQKLPSSRTICPGGSVAYGSCYSLILPQTW 60
QY 61 SNAELSCQHFSGHAFLLSTGEITFVSSLVKNLSITAYQYIMGLHPSHGTLPNSSGWR 120
DB 61 SNAELSCQHFSGHAFLLSTGEITFVSSLVKNLSITAYQYIMGLHPSHGTLPNSSGWR 120
QY 121 WSSSNVLTFFNNERNPSTADNGYCAVLSQKSGQKWRDNCENELPYICKFY 174
DB 121 WSSSNVLTFFNNERNPSTADNGYCAVLSQKSGQKWRDNCENELPYICKFY 174
RESULT 2
US-08-709-662-2
; Sequence 2, Application US/08709662
; Patent No. 5840531
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Pittenger, Gary L.
; APPLICANT: Rafaeloff, Ronit
; APPLICANT: Rosenberg, Lawrence
; APPLICANT: Duguid, William P.
; TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
ADDRESS: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-709-662-2

Query Match 100.0%; Score 174; DB 2; Length 174;
Best Local Similarity 100.0%; Pred. No.3,1e-171;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPTLCMSWMLSCLMFLSWVEGESOKKLPSSRITPCPGSVAYGSCYCSLLIPQW 60
DB 1 MLPTLCMSWMLSCLMFLSWVEGESOKKLPSSRITPCPGSVAYGSCYCSLLIPQW 60
QY 61 SNAELSCOMHPSGHLAFLSTGEITFFVSSLVKNLSITAYQYIWIIGLHDPHSGTLPNGSGWK 120
DB 61 SNAELSCOMHPSGHLAFLSTGEITFFVSSLVKNLSITAYQYIWIIGLHDPHSGTLPNGSGWK 120
QY 121 WSSSNVLTFFYNNRNPSTADRGYCAVLISOKSGFQKMRDNCENELPYICKFKV 174
DB 121 WSSSNVLTFFYNNRNPSTADRGYCAVLISOKSGFQKMRDNCENELPYICKFKV 174

RESULT 3
US-08-909-725-6
Sequence 6, Application US/08909725
Patent No. 5804421
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron
APPLICANT: Pittenger, Gary
APPLICANT: Rafaeloff-Phail, Ronlt
APPLICANT: Barlow, Scott
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: INGAIP IN BACTERIAL AND EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,725
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,096
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 0570.05173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

TELEX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-909-725-6

Query Match 100.0%; Score 174; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No.3,1e-171;
Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLPTLCMSWMLSCLMFLSWVEGESOKKLPSSRITPCPGSVAYGSCYCSLLIPQW 60
DB 2 MLPTLCMSWMLSCLMFLSWVEGESOKKLPSSRITPCPGSVAYGSCYCSLLIPQW 61
QY 61 SNAELSCOMHPSGHLAFLSTGEITFFVSSLVKNLSITAYQYIWIIGLHDPHSGTLPNGSGWK 120
DB 62 SNAELSCOMHPSGHLAFLSTGEITFFVSSLVKNLSITAYQYIWIIGLHDPHSGTLPNGSGWK 121
QY 121 WSSSNVLTFFYNNRNPSTADRGYCAVLISOKSGFQKMRDNCENELPYICKFKV 174
DB 122 WSSSNVLTFFYNNRNPSTADRGYCAVLISOKSGFQKMRDNCENELPYICKFKV 175

RESULT 4
US-08-909-725-5
Sequence 5, Application US/08909725
Patent No. 5804421
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron
APPLICANT: Pittenger, Gary
APPLICANT: Rafaeloff-Phail, Ronlt
APPLICANT: Barlow, Scott
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: INGAIP IN BACTERIAL AND EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,725
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,096
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 0570.05173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide


```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,156
; FILING DATE: 19911219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLION, No. 5436169man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 354-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 184 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-778-156-2

```

```

Query Match      5.7%; Score 10; DB 1; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 MSWMLISCLM 18
    |||||||
DB 10 MSWMLISCLM 19

```

```

RESULT 8
; Sequence 2, Application US/08422166
; Patent No. 5959086
; GENERAL INFORMATION:
; APPLICANT: IOVANNA, JUAN-LUCIO
; APPLICANT: KEIM, VOLKER
; APPLICANT: DAGORN, JEAN-CHARLES
; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
; TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
; TITLE OF INVENTION: PANCREATITIS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 Jefferson Davis Highway, Fourth floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,166
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/778,156
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLION, No. 5959086man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 354-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

```

```

; LENGTH: 184 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-422-166-2

```

```

Query Match      5.7%; Score 10; DB 2; Length 184;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 MSWMLISCLM 18
    |||||||
DB 10 MSWMLISCLM 19

```

```

Search completed: April 16, 2003, 10:51:09
Job time : 15 secs

```


GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 16, 2003, 10:49:31 ; Search time 19 seconds
(Without alignments)
692.464 Million cell updates/sec

Title: US-08-401-530-2

Perfect score: 174
Sequence: 1 MLEPTICRSMWLSLCLMTL.....QKWRDPCNCELPIYICKFRV 174

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 288829 seqs, 75613885 residues

Word size : 10

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep:*
2: /cgn2_6/ptodata/1/pubpaa/PT_NEM_PUB pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep:*
7: /cgn2_6/ptodata/1/pubpaa/PTUS_PUBCOMB pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep:*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep:*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep:*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	12.1	21	US-10-036-418-1	Sequence 1, Appli
2	15	8.6	15	US-10-036-418-2	Sequence 2, Appli
3	14	8.0	14	US-10-036-418-3	Sequence 3, Appli
4	14	8.0	14	US-10-036-418-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-036-418-1
; Sequence 1, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126 00009
; CURRENT APPLICATION NUMBER: US/10/036,418

CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Cricetus

US-10-036-418-1

Query Match 12.18; Score 21; DB 12; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 FLSWEGESOKRLPSRITC 39
DB 1 FLSWEGESOKRLPSRITC 21

RESULT 2
US-10-036-418-2

; Sequence 2, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:

; APPLICANT: Vinik, Aaron

; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126 00009

CURRENT APPLICATION NUMBER: US/10/036,418
CURRENT FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: 60/260,210
PRIOR FILING DATE: 2000-01-09

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2

LENGTH: 15
TYPE: PRT
ORGANISM: Cricetus

US-10-036-418-2

Query Match 8.64; Score 15; DB 12; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 103 IGLHPSHGTLPNGS 117
DB 1 IGLHPSHGTLPNGS 15

RESULT 3
US-10-036-418-3

; Sequence 3, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:

; APPLICANT: Vinik, Aaron

; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INGAP Displacement Assay
; FILE REFERENCE: 005126 00009

CURRENT APPLICATION NUMBER: US/10/036,418
CURRENT FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: 60/260,210
PRIOR FILING DATE: 2000-01-09

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3

LENGTH: 14
TYPE: PRT
ORGANISM: Cricetus

US-10-036-418-3

Query Match 8.08; Score 14; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 IAADRGYCAVLSQK 151
|||||
DB 1 IAADRGYCAVLSQK 14

RESULT 4

US-10-036-418-4
; Sequence 4, Application US/10036418
; Patent No. US20020127624A1
; GENERAL INFORMATION:
; APPLICANT: Vainik, Aaron
; APPLICANT: Taylor-Fishwick, David
; TITLE OF INVENTION: INCAP Displacement Assay
; FILE REFERENCE: 005126.00009
; CURRENT APPLICATION NUMBER: US/10/036,418
; CURRENT FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 60/260,210
; PRIOR FILING DATE: 2000-01-09
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Cricetus
US-10-036-418-4

Query Match 8.0%; Score 14; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 OKSGFOKWRDENCE 163
|||||
DB 1 OKSGFOKWRDENCE 14

Search completed: April 16, 2003, 10:51:34
Job time : 19 secs